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72025

From: Maupin, Christine
Sent: Monday, July 29, 2002 6:46 PM
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Subject: application 10/014743

Sensitivity: Private

could I please have the 3 sequences for application 10/014743 search in all data bases
thank you
Christine

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Point of Contact:
Beverly Shears
Technical Info. Specialist
CM1 1E05 Tel: 308-4994

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Searcher: _____
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Location: _____
Date Picked Up: _____
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH:

NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)

STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
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SEARCH REQUEST FORM

Requestor's Name: _____ Serial Number: _____
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Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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Date completed: 08-01-02
08-02-02
Searcher: Beverly C 4994
Terminal time: 20
Elapsed time: _____
CPU time: _____
Total time: 25
Number of Searches: _____
Number of Databases: 1

Search Site

____ STIC
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Type of Search

____ N.A. Sequence
____ A.A. Sequence
____ Structure
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☒ Other CGN

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 07:50:09 ; Search time 4897.61 Seconds
(without alignments)
5376.025 Million cell updates/sec

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues

Total number of hits satisfying chosen parameters: 43959072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1217	100.0	1217	11	US-08-726-462-1	Sequence 1, Appl
2	1217	100.0	1217	11	US-08-726-462A-1	Sequence 1, Appl
3	1217	100.0	1217	37	US-10-014-743-1	Sequence 1, Appl
C 4	1150.8	94.6	7294	1	PCT-US93-10850-1	Sequence 5, Appl
C 5	1150.8	94.6	7294	1	PCT-US93-10850-5	Sequence 1, Appl
C 6	1150.8	94.6	7294	5	US-08-150-740-1	Sequence 5, Appl
C 7	1150.8	94.6	7294	5	US-08-150-740-5	Sequence 1, Appl
C 8	1150.8	94.6	7294	8	US-08-440-787-1	Sequence 5, Appl
C 9	1150.8	94.6	7294	8	US-08-440-787-5	Sequence 1, Appl
C 10	1150.8	94.6	7294	13	US-08-995-243-1	Sequence 5, Appl
C 11	1150.8	94.6	7294	13	US-08-995-243A-1	Sequence 1, Appl
C 12	1150.8	94.6	7294	13	US-08-995-243A-5	Sequence 5, Appl
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C 14	1150.8	94.6	7294	29	US-09-727-311-5	Sequence 5, Appl
C 15	1140.4	93.7	7083	1	PCT-US99-18207-1	Sequence 1, Appl
C 16	1140.4	93.7	7083	22	US-09-562-836-1	Sequence 1, Appl
C 17	1140.4	93.7	7083	36	US-09-995-396-1	Sequence 2, Appl
C 18	1140.4	93.7	7083	8	US-08-470-297-2	Sequence 2, Appl
C 19	1131.4	93.0	7317	8	US-08-471-622-2	Sequence 2, Appl
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C 21	1131.4	93.0	7320	5	PCT-US93-10850-2	Sequence 2, Appl
C 22	1131.4	93.0	7320	5	US-08-150-740-2	Sequence 2, Appl
C 23	1131.4	93.0	7320	8	US-08-440-787-2	Sequence 2, Appl
C 24	1131.4	93.0	7320	13	US-08-995-243-2	Sequence 2, Appl
C 25	1131.4	93.0	7320	13	US-08-995-243A-2	Sequence 2, Appl
C 26	1131.4	93.0	7320	29	US-09-727-311-2	Sequence 2, Appl
C 27	1131.4	93.0	7320	29	US-09-727-311-5	Sequence 4, Appl
C 28	1131.4	93.0	7557	8	US-08-470-297-4	Sequence 4, Appl
C 29	1131.4	93.0	7557	8	US-08-471-622A-4	Sequence 4, Appl
C 30	1131.4	93.0	7557	8	US-08-471-622A-4	Sequence 4, Appl
C 31	1131.4	93.0	8118	8	US-08-470-297-5	Sequence 5, Appl

Maupin
10:014743
Seq. IDs 1-3 w/notes

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ALIGNMENTS

RESULT 1
 US-08-726-462-1
 ; Sequence 1, Application US/08726462
 ; GENERAL INFORMATION:
 ; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
 ; APPLICANT: Division
 ; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED
 ; TITLE OF INVENTION: FLUORESCENCE
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
 ; & Rosati
 ; STREET: 650 Page Mill Road
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94304-1050
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch diskette
 ; COMPUTER: IBM compatible
 ; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
 ; SOFTWARE: Wordperfect for windows 6.0,
 ; ASCII (DOS) TEXT format
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/726,462
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/642,330
 ; FILING DATE: May 3, 1996
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/672,196
 ; FILING DATE: June 27, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: David J. Weitz
 ; REGISTRATION NUMBER: 38,362
 ; REFERENCE/DOCKET NUMBER: PELM4304
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 493-9300
 ; TELEFAX: (415) 493-6811
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1217 nucleotides
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-726-462-1

Query Match 100.0%; Score 1217; DB 11; Length 1217;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1201 CATTCTGGCCACACAG 1217

RESULT 3
US-10-014-743-1
; Sequence 1, Application US/10014743
; GENERAL INFORMATION:
; APPLICANT: PE Corporation (NY)
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; APPLICATION NUMBER: 08/726,462
; FILING DATE: October 4, 1996
; APPLICATION NUMBER: 09/046,203
; FILING DATE: March 23, 1998
; APPLICATION NUMBER: 09/272,097
; FILING DATE: March 18, 1999
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: 16842-776
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 493-9300
; TELEFAX: (650) 493-6811
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-014-743-1

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	6226	ATCCTGGTCATAGCTGTTTCCTGCTGTGAAATTTGTTATCCGCTCACAATTCACACACAT	6167	
* QY	124	ACGAGCCGAAGCATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGCTAACTCACATT	183	
Db	6166	ACGAGCCGAAGCATAAAGTGTAAAGCCTGGGTGCTTAATGAGTGAGCTAACTCACATT	6107	
QY	184	AATTGGGTTGCGCTCACTGCCGCTTTCAGTCGGGAAACCTGTCGTGCCAGTGCATTA	243	
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Db	6046	ATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGCTATTGGCGGCCAGGGTGGTTTTTC	5987	
QY	304	TTTTCAACAGTGAGACGGGCAACAGCTGATTCGCCCTTCACCGCCTGGCCCTGAGAGATT	363	
Db	5986	TTTTCAACAGCGAGACGGGCAACAGCTGATTCGCCCTTCACCGCCTGGCCCTGAGAGATT	5927	
QY	364	CGACGACGGTCCACGCTGTTTTGCCCGCAGCAGCGGAAATCCTGTTGATGGTGGTTC	423	
Db	5926	CGACGACGGTCCACGCTGTTTTGCCCGCAGCAGCGGAAATCCTGTTGATGGTGGTTC	5867	
QY	424	CGAAATCGGCAAAATCCCTTATAATCAAAAGAAATAGCCCGAGATGAGGTTGAGTGTGT	483	
Db	5866	CGAAATCGGCAAAATCCCTTATAATCAAAAGAAATAGCCCGAGATGAGGTTGAGTGTGT	5807	
QY	484	TCCAGTTGGGAACAGAGTCCACTATTAAAGAACGTGGACTCCAAAGTCAAGGCGGAAA	543	
Db	5806	TCCAGTTGGGAACAGAGTCCACTATTAAAGAACGTGGACTCCAAAGTCAAGGCGGAAA	5747	
QY	544	AACCGTCTATCAGGGCGATGCCACATACGTGAACCATCACCCAAATCAAGTTTTTGGG	603	
Db	5746	AACCGTCTATCAGGGCGATGCCACATACGTGAACCATCACCCAAATCAAGTTTTTGGG	5687	
QY	604	GTGAGGTGCGGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCGCATTTAGAGCTTG	663	
Db	5686	GTGAGGTGCGGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCGCATTTAGAGCTTG	5627	
QY	664	ACGGGAAAGCCGGCAACCTGGCGAGAAAGGAGGAAACGGAAGAGCGGCGCG	723	
Db	5626	ACGGGAAAGCCGGCAACCTGGCGAGAAAGGAGGAAAGGAGGAAAGGAGCGGCGCG	5567	

964 GTCCATCAGCAAAATTAACGGTTGTAGCAATACCTCTTTGATTAGTAATAACATCACTTG 1023
5326 GTCCATCAGCAAAATTAACGGTTGTAGCAATACCTCTTTGATTAGTAATAACATCACTTG 5267
1024 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTCTGTAATATATCCAGAACATATACCGC 1083
5266 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTCTGTAATATATCCAGAACATATACCGC 5207
1084 CAGCATTCAGCAAGGAAACGCTCATGAAATACCTACATTTTGACGCTCAATCGTCT 1143
5206 CAGCATTCAGCAAGGAAACGCTCATGAAATACCTACATTTTGACGCTCAATCGTCT 5147
1144 GAAATGATTTATTTACATTTGGCAGATTCACAGTCACACGACAGTAATTAAGGGGACAT 1203
5146 GAAATGATTTATTTACATTTGGCAGATTCACAGTCACACGACAGTAATTAAGGGGACAT 5087
1204 TCTGCCCAACAGAG 1217
5086 TCTGCCCAACAGAG 5073

64 ATCATGTCATAGCTGTTTCTCTGTTGAAATGTTATCGCTCAAAATTCACACAAAT 123
6226 ATCTGTCATAGCTGTTTCTCTGTTGAAATGTTATCGCTCAAAATTCACACAAAT 6167
124 ACAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTCCCTAATGAGTGAGTCACTCAAT 183
6166 ACAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTCCCTAATGAGTGAGTCACTCAAT 6107
184 AATTCGCTGCGCTACTCCCGCTTTCCAGTCGGAACCTGCTGTCGACGCTCAAT 243
6106 AATTCGCTGCGCTACTCCCGCTTTCCAGTCGGAACCTGCTGTCGACGCTCAAT 6047
244 ATCAATCGCCACGCGCGGAGAGCGGTTTGCCTATTTGGCGCCAGGGTGGTTTC 303
6046 ATCAATCGCCACGCGCGGAGAGCGGTTTGCCTATTTGGCGCCAGGGTGGTTTC 5987
304 TTTTCCAGTGTAGAGCGGCAACAGCTGATGTCCTTACCCTGCGCTGAGAGAGTT 363
5986 TTTTCCAGTGTAGAGCGGCAACAGCTGATGTCCTTACCCTGCGCTGAGAGAGTT 5927
364 GCAGCAGCGCTCCAGCTGTTTGGCCAGCAGGCGAAATCCTGTTGATGGTGGTTC 423
5926 GCAGCAGCGCTCCAGCTGTTTGGCCAGCAGGCGAAATCCTGTTGATGGTGGTTC 5867
424 CGAATCGGCAAAATCCCTTATATAATCAAAAGATAGCCCGAGATGGTGGTGT 483
5866 CGAATCGGCAAAATCCCTTATATAATCAAAAGATAGCCCGAGATGGTGGTGT 5807
484 TCCAGTTTGGAGACAGTCCACATTAATAAGAACGTCGAGCTCCAAAGCGCGAAA 543
5806 TCCAGTTTGGAGACAGTCCACATTAATAAGAACGTCGAGCTCCAAAGCGCGAAA 5747
544 AACCTCTATCAGGCGGATGCCCACTACGTTGAACCATCACCCCAATCAAGTTTGGG 603
5746 AACCTCTATCAGGCGGATGCCCACTACGTTGAACCATCACCCCAATCAAGTTTGGG 5687
604 GTCGAGGTGCGGTAAGCACTAAATCGGAACCTAAAGGAGCGCCCGGATTTAGAGCTTG 663
5686 GTCGAGGTGCGGTAAGCACTAAATCGGAACCTAAAGGAGCGCCCGGATTTAGAGCTTG 5627
664 ACAGGAAAGCGCGGCAACGTCGCGAGAAAGGAGGAGAAAGGAGGAGCGCGGC 723
5626 ACAGGAAAGCGCGGCAACGTCGCGAGAAAGGAGGAGAAAGGAGGAGCGCGGC 5567
724 TAGGGCGCTGGAAGTGTAGCGGTACGCTGCGCTGACGCTAACCCACCGCGCTTAA 783
5566 TAGGGCGCTGGAAGTGTAGCGGTACGCTGCGCTGACGCTAACCCACCGCGCTTAA 5507
784 TGGCGCGCTACAGGCGCGTACTATGTTGTTTGTAGAGCAGTATACGCTTCTCT 843
5506 TGGCGCGCTACAGGCGCGTACTATGTTGTTTGTAGAGCAGTATACGCTTCTCT 5447
844 CGTTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGATTTTAGACAGGAACG 903
5446 CGTTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGATTTTAGACAGGAACG 5387
904 GTAGCCAGAAATCTTGAGAGTGTGTTTATATATCAGTGAGGCGCCAGGTAAGAGTCT 963
5386 GTAGCCAGAAATCTTGAGAGTGTGTTTATATATCAGTGAGGCGCCAGGTAAGAGTCT 5327

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 7294 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
US-08-150-740-1

Query Match 94.6%; Score 1150.8; DB 5; Length 7294;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 7

US-08-150-740-5/C
Sequence 5, Application US/08150740
GENERAL INFORMATION:
APPLICANT: Huse, William D.
TITLE OF INVENTION: Soluble Peptides Having Constrained,
TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
TITLE OF INVENTION: Same.
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/150,740
FILING DATE: 10-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,893
FILING DATE: 10-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kanski, Antoinette F.
REGISTRATION NUMBER: 34,202
REFERENCE/DOCKET NUMBER: P-IX 9796
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7294 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
US-08-150-740-5

Query Match 94.6%; Score 1150.8; DB 5; Length 7294;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
64 ATCATGTCATAGCTGTTTCTCTGTTGAAATGTTATCGCTCAAAATTCACACAAAT 123
6226 ATCTGTCATAGCTGTTTCTCTGTTGAAATGTTATCGCTCAAAATTCACACAAAT 6167
Db

QY 124 ACGAGCCGGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTGAGCTAACATCACATT 183
Db 6166 ACGAGCCGGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTGAGCTAACATCACATT 6107
QY 184 AATTGCGTTGCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGCTGCTGCCAGCTGCATTA 243
Db 6106 AATTGCGTTGCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGCTGCTGCCAGCTGCATTA 6047
QY 244 ATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGGTATTTGGGCGCCAGGCTGGTTTTTC 303
Db 6046 ATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGGTATTTGGGCGCCAGGCTGGTTTTTC 5987
QY 304 TTTTCCAGCTGAGAGCGGCAACAGCTGATTTGCCCTTCCAGCCCTGGCCCTGAGAGAGTT 363
Db 5986 TTTTCCAGCTGAGAGCGGCAACAGCTGATTTGCCCTTCCAGCCCTGGCCCTGAGAGAGTT 5927
QY 364 GCAGCAAGCGTCCAGCGTGGTTTGGCCCGAGCGGCAAAATCCTGTTGATGGTGGTTC 423
Db 5926 GCAGCAAGCGTCCAGCGTGGTTTGGCCCGAGCGGCAAAATCCTGTTGATGGTGGTTC 5867
QY 424 CGAAATCGGCAAAATCCTTATAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 483
Db 5866 CGAAATCGGCAAAATCCTTATAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 5807
QY 484 TCCAGTTTGAACAAGAGTCCACTATTAAAGACGTGAGTCCCACTGCAAGGCGGAA 543
Db 5806 TCCAGTTTGAACAAGAGTCCACTATTAAAGACGTGAGTCCCACTGCAAGGCGGAA 5747
QY 544 AACCGTCTATCAGGCGGATGGCCGCTAGCTGAACCATCACCCAAATCAAGTTTGGG 603
Db 5746 AACCGTCTATCAGGCGGATGGCCGCTAGCTGAACCATCACCCAAATCAAGTTTGGG 5687
QY 604 GTGAGTGGCGTAAAGCACTAATCGGAACCTTAAGGAGAGCCCGGATTTAGAGTTG 663
Db 5686 GTGAGTGGCGTAAAGCACTAATCGGAACCTTAAGGAGAGCCCGGATTTAGAGTTG 5627
QY 664 ACGGGAAAGCGGCGGAGTGGCGGAGAAAGGAAGGAAAGCAAGGAGGAGCGGCGC 723
Db 5626 ACGGGAAAGCGGCGGAGTGGCGGAGAAAGGAAGGAAAGCAAGGAGGAGCGGCGC 5567
QY 724 TAGGCGCTGGCAAGTGTAGCGGTGACGTGCGCGTAAACCAACACACCGCGCGCTTAA 783
Db 5566 TAGGCGCTGGCAAGTGTAGCGGTGACGTGCGCGTAAACCAACACACCGCGCGCTTAA 5507
QY 784 TCGCGCGCTACAGCGCGGTACTATGTTGCTTTGACGAGCAGTATAACGTCTTCT 843
Db 5506 TCGCGCGCTACAGCGCGGTACTATGTTGCTTTGACGAGCAGTATAACGTCTTCT 5447
QY 844 CTTTGGAAATCAGAGCGGAGCTTAAACAGGAGCGGCTTAAAGGGAATTTAGACGAAG 903
Db 5446 CTTTGGAAATCAGAGCGGAGCTTAAACAGGAGCGGCTTAAAGGGAATTTAGACGAAG 5387
QY 904 GTACGCGAATCTTGAGAGTGTATTAATCAGTGAGGCGCCAGGAGTAAAGAGTCT 963
Db 5386 GTACGCGAATCTTGAGAGTGTATTAATCAGTGAGGCGCCAGGAGTAAAGAGTCT 5327
QY 964 GTCCATCAGCAAAATTAACCGTTGAGCAATCTTTGATTTAGTATAACATCATTG 1023
Db 5326 GTCCATCAGCAAAATTAACCGTTGAGCAATCTTTGATTTAGTATAACATCATTG 5267
QY 1024 CTTGAGTAGAAGAACTCAAACTATCGCCCTTGTGTTGATTAATCCAGAACATATACCG 1083
Db 5266 CTTGAGTAGAAGAACTCAAACTATCGCCCTTGTGTTGATTAATCCAGAACATATACCG 5207
QY 1084 CAGCCATTGCAACAGGAAACCTCATGGAATACCTACATTTTACGCTCAATCGTCT 1143
Db 5206 CAGCCATTGCAACAGGAAACCTCATGGAATACCTACATTTTACGCTCAATCGTCT 5147
QY 1144 GAATGGATTTTACATTTGGCAGATTTACAGCTCACAGCAGCAATTAAGAGGACAT 1203
Db 5146 GAATGGATTTTACATTTGGCAGATTTACAGCTCACAGCAGCAATTAAGAGGACAT 5087
QY 1204 TCTGGCCAAACAGAG 1217

Db 5086 TCTGGCCAAACAGAG 5073

RESULT 8

US-08-440-787-1/c
; Sequence 1, Application US/08440787
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SOLUBLE PEPTIDES HAVING CONSTRAINED, SECONDARY
; TITLE OF INVENTION: CONFORMATION IN SOLUTION AND METHOD OF MAKING SAME
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, STE #700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC Compatible
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440.787
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/07/978.893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: P-IX 9382
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 1:
; LENGTH: 7294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-440-787-1

Query Match 94.6%; Score 1150.8; DB 8; Length 7294;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATGGTCATAGCTCTTTCCTGCTGTAATTTCCGCTCACAATTTCCACACACAT 123
Db 6226 ATCTCTGGTCATAGCTCTTTCCTGCTGTAATTTCCGCTCACAATTTCCACACACAT 6167
QY 124 ACGAGCCGGAACGATTAAGTGTAAAGCCCTGGGCTGCTTAATGAGTGAGCTAACATCAATT 183
Db 6166 ACGAGCCGGAACGATTAAGTGTAAAGCCCTGGGCTGCTTAATGAGTGAGCTAACATCAATT 6107
QY 184 AATTGCGTTGCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGCTGCTGCCAGCTGCATTA 243
Db 6106 AATTGCGTTGCGCTCACTGCGCGCTTTCCAGTCGGGAAACCTGCTGCTGCCAGCTGCATTA 6047
QY 244 ATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGGTATTTGGGCGCCAGGCTGGTTTTTC 303
Db 6046 ATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGGTATTTGGGCGCCAGGCTGGTTTTTC 5987
QY 304 TTTTCCAGCTGAGAGCGGCAACAGCTGATTTGCCCTTCCAGCCCTGGCCCTGAGAGAGTT 363
Db 5986 TTTTCCAGCTGAGAGCGGCAACAGCTGATTTGCCCTTCCAGCCCTGGCCCTGAGAGAGTT 5927
QY 364 GCAGCAAGCGTCCAGCGTGGTTTGGCCCGAGCGGCAAAATCCTGTTGATGGTGGTTC 423
Db 5926 GCAGCAAGCGTCCAGCGTGGTTTGGCCCGAGCGGCAAAATCCTGTTGATGGTGGTTC 5867

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5926 GCAGCAAGCGTCCACGCTGGTTTGGCCCGAGCGGAAATCCTGTTGATGGTGGTTC 5867
Db
QY 424 CGAAATCGCAAAATCCCTTATAAATCAAAAGAAATACGCCGAGATAGGGTTGAGTGTGT 483
Db 5866 CGAAATCGCAAAATCCCTTATAAATCAAAAGAAATACGCCGAGATAGGGTTGAGTGTGT 5807
QY 484 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTTGGATCTCAACGCTCAAGGGCGAAA 543
Db 5806 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTTGGATCTCAACGCTCAAGGGCGAAA 5747
QY 544 ACCGCTCTATCAGGGGATGGCCCACTACGTGAACATCAACCAATCAAGTTTGGG 603
Db 5746 AACCGCTCTATCAGGGGATGGCCCACTACGTGAACATCAACCAATCAAGTTTGGG 5687
QY 604 GTCGAGTGGCGTAAAGCACTAAATCGAAACCTTAAAGGAGCGCCCGATTTAGAGTTG 663
Db 5686 GTCGAGTGGCGTAAAGCACTAAATCGAAACCTTAAAGGAGCGCCCGATTTAGAGTTG 5627
QY 664 ACAGGAAACCGCGCAACGTTGGGAGAAAGAAAGGAAAGCAAGCGAGCGGCG 723
Db 5626 ACAGGAAACCGCGCAACGTTGGGAGAAAGGAAAGGAAAGCAAGCGAGCGGCG 5567
QY 724 TAGGCGCTGGCAGTGTAGCGTACGCTGCGGTAAACCAACACCGCGCGCTTAA 783
Db 5566 TAGGCGCTGGCAGTGTAGCGTACGCTGCGGTAAACCAACACCGCGCGCTTAA 5507
QY 784 TGCSCCGCTACAGGCGCGTACTATGTTGTTTGAAGAGCAGCTATAACGTGTTTCT 843
Db 5506 TGCSCCGCTACAGGCGCGTACTATGTTGTTTGAAGAGCAGCTATAACGTGTTTCT 5447
QY 844 CGTTGGAATCAGCGGGAGCTAAACAGGCGCGATTAAGGGGATTTAGACAGCAAG 903
Db 5446 CGTTGGAATCAGCGGGAGCTAAACAGGCGCGATTAAGGGGATTTAGACAGCAAG 5387
QY 904 GTACGCCAGATCTTGAGAGTGTGTTTATATCAAGTGAAGCGCCAGTAAAGAGTCT 963
Db 5386 GTACGCCAGATCTTGAGAGTGTGTTTATATCAAGTGAAGCGCCAGTAAAGAGTCT 5327
QY 964 GTCCATCAGCAAAATTAACCGTTGAGCAATCTTCTTGATTAACATCAATCACTTTG 1023
Db 5326 GTCCATCAGCAAAATTAACCGTTGAGCAATCTTCTTGATTAACATCAATCACTTTG 5267
QY 1024 CCGAGTAGAAGAACTCAAACTATCGGCTTCTGTTGATTAACATCAATCACTTTG 1083
Db 5266 CCGAGTAGAAGAACTCAAACTATCGGCTTCTGTTGATTAACATCAATCACTTTG 5207
QY 1084 CAGCCATTGCAACAGAAACCGCTCATGGAATACCTACATTTGACGCTCAATCGTCT 1143
Db 5206 CAGCCATTGCAACAGAAACCGCTCATGGAATACCTACATTTGACGCTCAATCGTCT 5147
QY 1144 GAAATGGATTATTACATTGGCAGATTACAGTCAACGAGCAGTAAATAAGGGGACAT 1203
Db 5146 GAAATGGATTATTACATTGGCAGATTACAGTCAACGAGCAGTAAATAAGGGGACAT 5087
QY 1204 TCTGGCCAAACAGAG 1217
Db 5086 TCTGGCCAAACAGAG 5073

RESULT 9
US-08-440-787-5/c
; Sequence 5, Application US/08440787
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SOLUBLE PEPTIDES HAVING CONSTRAINED, SECONDARY
; TITLE OF INVENTION: CONFORMATION IN SOLUTION AND METHOD OF MAKING SAME
; NUMBER OF SEQUENCES: 64
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL AND FLORES
; STREET: 4370 LA JOLLA VILLAGE DRIVE, STE #700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: U.S.A.

ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,787
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/978,893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: KOSKI, ANTOINETTE F.
; REGISTRATION NUMBER: 34,202
; REFERENCE/DOCKET NUMBER: P-IX 9382
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-440-787-5

Query Match 94.68; Score 1150.8; DB 8; Length 7294;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 64 ATCATGCTCATAGCTGTTTCCTGTGTGAAATTTGTTATCCGCTCACAATTCACACAACAT 123
Db 6226 ATGCTGCTCATAGCTGTTTCCTGTGTGAAATTTGTTATCCGCTCACAATTCACACAACAT 6167
QY 124 ACAGCGCGAAGCATAAAGTGTAAAGCTGGGTGGCTTAATGAGTGAAGTAACTACACATT 183
Db 6166 ACAGCGCGAAGCATAAAGTGTAAAGCTGGGTGGCTTAATGAGTGAAGTAACTACACATT 6107
QY 184 AATTTGCTTCGCTCACTGCGCGCTTCCAGTTCGGGAAACCTGCTGTCGCCAGCTGCAATTA 243
Db 6106 AATTTGCTTCGCTCACTGCGCGCTTCCAGTTCGGGAAACCTGCTGTCGCCAGCTGCAATTA 6047
QY 244 ATGAATCGGCCAACGCGCGGGGAGAGCGGTTTCGCTATTGGGCGCCAGGGTGTGTTTC 303
Db 6046 ATGAATCGGCCAACGCGCGGGGAGAGCGGTTTCGCTATTGGGCGCCAGGGTGTGTTTC 5987
QY 304 TTTTCACGAGTGAAGCGGCAACAGCTGATTGCCCTTCCAGCTGCGCCCTGGCCCTGAGAGATT 363
Db 5986 TTTTCACGAGTGAAGCGGCAACAGCTGATTGCCCTTCCAGCTGCGCCCTGGCCCTGAGAGATT 5927
QY 364 GCACAAAGCGGTCCACAGCTGTTTGGCCCGCAGCGGAAATTCCTGTTGATGTTGTTTC 423
Db 5926 GCACAAAGCGGTCCACAGCTGTTTGGCCCGCAGCGGAAATTCCTGTTGATGTTGTTTC 5867
QY 424 CGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCGAGATAGGTTGAGTGTGT 483
Db 5866 CGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCGAGATAGGTTGAGTGTGT 5807
QY 484 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTTGGATCTCAACGCTCAAGGGCGAAA 543
Db 5806 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTTGGATCTCAACGCTCAAGGGCGAAA 5747
QY 544 AACCGCTCTATCAGGGGATGGCCCACTACGTGAACATCAACCAATCAAGTTTGGG 603
Db 5746 AACCGCTCTATCAGGGGATGGCCCACTACGTGAACATCAACCAATCAAGTTTGGG 5687
QY 604 GTCGAGTGGCGTAAAGCACTAAATCGAAACCTTAAAGGAGCGCCCGATTTAGAGTTG 663
Db 5686 GTCGAGTGGCGTAAAGCACTAAATCGAAACCTTAAAGGAGCGCCCGATTTAGAGTTG 5627

Db 5386 GTACGCCAGAATCTTTGAGAAGTGTATTAATCAGTGTGAGCCACCGAGTAAAGAGTCT 5327
 Qy 964 GTCCATACAGCAAAATTAACCGTTGTAGCAATACCTTTCTTTGATAGTAAATACATCAGTTG 1023
 Db 5326 GTCCATACAGCAAAATTAACCGTTGTAGCAATACCTTTCTTTGATAGTAAATACATCAGTTG 5267
 Qy 1024 CCTGAGTAGAAGAACTCAAACTATCGGCTTGTCTGTAATATCCAGAACAAATATACCGC 1083
 Db 5266 CCTGAGTAGAAGAACTCAAACTATCGGCTTGTCTGTAATATCCAGAACAAATATACCGC 5207
 Qy 1084 CAGCCATTCACAGCAAAACCGCTCATGGAATACCTACATTTTGAAGCTCAATCGTCT 1143
 Db 5206 CAGCCATTCACAGCAAAACCGCTCATGGAATACCTACATTTTGAAGCTCAATCGTCT 5147
 Qy 1144 GAAATGGATTTATACATTTGGAGATTCACAGCACAGCAATTAATAAAGGACAT 1203
 Db 5146 GAAATGGATTTATACATTTGGAGATTCACAGCACAGCAATTAATAAAGGACAT 5087
 Qy 1204 TCTGGCCACAGAG 1217
 Db 5086 TCTGGCCACAGAG 5073

RESULT 11

US-08-995-243-5/C
 ; Sequence 5, Application US/08995243
 ; GENERAL INFORMATION:
 ; APPLICANT: HUSE, WILLIAM D.
 ; TITLE OF INVENTION: SOLUBLE PEPTIDES HAVING CONSTRAINED, SECONDARY
 ; TITLE OF INVENTION: CONFORMATION IN SOLUTION AND METHOD OF MAKING SAME
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CAMPBELL AND FLORES
 ; STREET: 4370 LA JOLLA VILLAGE DRIVE, STE #700
 ; CITY: SAN DIEGO
 ; STATE: CALIFORNIA
 ; COUNTRY: U.S.A.
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/995,243
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/978,893
 ; FILING DATE: 10-NOV-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: KONSKI, ANTOINETTE F.
 ; REGISTRATION NUMBER: 34,202
 ; REFERENCE/DOCKET NUMBER: P-IX 9382
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 619-535-9001
 ; TELEFAX: 619-535-8949
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: circular
 ; US-08-995-243-5

Query Match 94.6%; Score 1150.8; DB 13; Length 7294;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 64 ATCATGGTCATAGCTGTTTCTGTTGTAATGTTATCCGCTCAAAATTCACACAAACAT 123
 Db 6226 ATCCCTGGTCATAGCTGTTTCTGTTGTAATGTTATCCGCTCAAAATTCACACAAACAT 6167

Qy 124 ACAGAGCGGAGCAATAAAGTGTAAAGCCTGGGTGCCTAATAGTGTAGCTAACTCAAT 183
 Db 6166 ACAGAGCGGAGCAATAAAGTGTAAAGCCTGGGTGCCTAATAGTGTAGCTAACTCAAT 6107
 Qy 184 AATTGCGTTGGCTCACTGCCCGCTTTCCAGTTCGGGAAACCTGTCTGCCAGCTGCATTA 243
 Db 6106 AATTGCGTTGGCTCACTGCCCGCTTTCCAGTTCGGGAAACCTGTCTGCCAGCTGCATTA 6047
 Qy 244 ATGAATCGCCCAACCGCGGGGAGAGGGGTTTGGTATTTGGGCGCCAGGCTGTTTTC 303
 Db 6046 ATGAATCGCCCAACCGCGGGGAGAGGGGTTTGGTATTTGGGCGCCAGGCTGTTTTC 5987
 Qy 304 TTTTCCACAGTGTAGAGCGGCAACAGCTGATTCCTTCCACCGCTTGGCCCTGTGAGAGATT 363
 Db 5986 TTTTCCACAGTGTAGAGCGGCAACAGCTGATTCCTTCCACCGCTTGGCCCTGTGAGAGATT 5927
 Qy 364 GCAGCAAGCGTTCACAGCTGTGTTGCCCGCAGCAGCGGAAATCTGTTGATGTTGTTTC 423
 Db 5926 GCAGCAAGCGTTCACAGCTGTGTTGCCCGCAGCAGCGGAAATCTGTTGATGTTGTTTC 5867
 Qy 424 CGAAATCGGCAAAATCCCTTATATAAATCAAAAGAAATAGCCGAGATAGGTTGTTGT 483
 Db 5866 CGAAATCGGCAAAATCCCTTATATAAATCAAAAGAAATAGCCGAGATAGGTTGTTGT 5807
 Qy 484 TCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAAGCTCAAGGGCGAAA 543
 Db 5806 TCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAAGCTCAAGGGCGAAA 5747
 Qy 544 AACCGTCTATCAGGCGGATGGCCCTTACCTGAAACATACCCCAATCAAGTTTGTGGG 603
 Db 5746 AACCGTCTATCAGGCGGATGGCCCTTACCTGAAACATACCCCAATCAAGTTTGTGGG 5687
 Qy 604 GTGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAGAGGAGCCCGATTTAGAGCTTG 663
 Db 5686 GTGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAGAGGAGCCCGATTTAGAGCTTG 5627
 Qy 664 ACAGGGAAGCGCGGCAACGTGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 723
 Db 5626 ACAGGGAAGCGCGGCAACGTGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5567
 Qy 724 TAGGCGCTGCGCAAGTGTAGCGGTACAGCTGCGGTAAACACACACACCCCGCGCTTAA 783
 Db 5566 TAGGCGCTGCGCAAGTGTAGCGGTACAGCTGCGGTAAACACACACACCCCGCGCTTAA 5507
 Qy 784 TCGCGCTACAGGCGCGTACTATGTTGCTTTGACGAGCAGCTATACCTGCTTCTCT 843
 Db 5506 TCGCGCTACAGGCGCGTACTATGTTGCTTTGACGAGCAGCTATACCTGCTTCTCT 5447
 Qy 844 CGTTGGAATCAGAGCGGAGCTTAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 903
 Db 5446 CGTTGGAATCAGAGCGGAGCTTAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5387
 Qy 904 GTACGCCAGAATCTTGAGAAGTGTATTAATCAGTGTAGGCGCCAGCTTAAAGAGTCT 963
 Db 5386 GTACGCCAGAATCTTGAGAAGTGTATTAATCAGTGTAGGCGCCAGCTTAAAGAGTCT 5327
 Qy 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATACCTTTCTTTGATAGTAAATACATCAGTTG 1023
 Db 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATACCTTTCTTTGATAGTAAATACATCAGTTG 5267
 Qy 1024 CCTGAGTAGAAGAACTCAAACTATCGGCTTGTCTGTAATATCCAGAACAAATATACCGC 1083
 Db 5266 CCTGAGTAGAAGAACTCAAACTATCGGCTTGTCTGTAATATCCAGAACAAATATACCGC 5207
 Qy 1084 CAGCCATTCACAGCAAAACCGCTCATGGAATACCTACATTTTGAAGCTCAATCGTCT 1143
 Db 5206 CAGCCATTCACAGCAAAACCGCTCATGGAATACCTACATTTTGAAGCTCAATCGTCT 5147
 Qy 1144 GAAATGGATTTATACATTTGGAGATTCACAGCACAGCAATTAATAAAGGACAT 1203
 Db 5146 GAAATGGATTTATACATTTGGAGATTCACAGCACAGCAATTAATAAAGGACAT 5087

QY 1204 TCTGGCCACACAGAG 1217
 DB 5086 TCTGGCCACACAGAG 5073

RESULT 12

US-08-995-243A-1/c
 ; Sequence 1, Application US/08995243A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Soluble Peptides Having Constrained,
 ; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
 ; NUMBER OF SEQUENCES: 174
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Campbell & Flores LLP
 ; STREET: 4370 La Jolla Village Drive, Suite 700
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92122
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/995,243A
 ; FILING DATE: 19-DEC-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/978,893
 ; FILING DATE: 10-NOV-1992
 ; APPLICATION NUMBER: US 08/440,787
 ; FILING DATE: 15-MAY-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A.
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P-1X 2955
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: circular
 ; US-08-995-243A-1

Query Match 94.6%; Score 1150.8; DB 13; Length 7294;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATGGTCATAGCTGTTTCTGCTGTAAGCTGGGTCCTTAATGAGTGAGCTAACTCACAAT 123
 DB 6226 ATCTGGTCATAGCTGTTTCTGCTGTAAGCTGGGTCCTTAATGAGTGAGCTAACTCACAAT 6167

QY 124 ACAGCCGGAAGCATAAGCTGTAAGCTGGGTCCTTAATGAGTGAGCTAACTCACAAT 183
 DB 6166 ACAGCCGGAAGCATAAGCTGTAAGCTGGGTCCTTAATGAGTGAGCTAACTCACAAT 6107

QY 184 AATTGCGTTGCGCTCACTGCGCGCTTCCAGTCGGAACCTGCTGCGTCCAGTGCATTA 243
 DB 6106 AATTGCGTTGCGCTCACTGCGCGCTTCCAGTCGGAACCTGCTGCGTCCAGTGCATTA 6047

QY 244 ATGAATCGGCAACGCGCGGAGAGCGGTTTTCGTTATTTGGCGCGAGGTTGTTTC 303
 DB 6046 ATGAATCGGCAACGCGCGGAGAGCGGTTTTCGTTATTTGGCGCGAGGTTGTTTC 5987

QY 304 TTTTACCACTGAGACGGCGCAACAGCTGATTGCCCTTACCGCTGCGCTGAGAGATT 363
 DB 5086 TCTGGCCACACAGAG 5073

RESULT 13
 US-08-995-243A-5/c
 ; Sequence 5, Application US/08995243A
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: Soluble Peptides Having Constrained,
 ; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
 ; NUMBER OF SEQUENCES: 174
 ; CORRESPONDENCE ADDRESS:

DB 5986 TTTTCAACAGCAGAGAGCGGCAACAGCTGATTGCCCTTCAACCGCCTGGCCCTGAGAGATT 5927
 QY 364 GCAGCAAGCGGTCACAGCTGTTTGGCCCGCAGAGCGGAAATCCTCTTTGATGGTGGTTC 423
 DB 5926 GCAGCAAGCGGTCACAGCTGTTTGGCCCGCAGAGCGGAAATCCTCTTTGATGGTGGTTC 5867
 QY 424 CGAATCGGCAAAATCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 483
 DB 5866 CGAATCGGCAAAATCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 5807
 QY 484 TCCAGTTTGAACAAGAGTCCACTATTAAAGAAGCTGACCTCCAACTGTCGAAAGGCGGAA 543
 DB 5806 TCCAGTTTGAACAAGAGTCCACTATTAAAGAAGCTGACCTCCAACTGTCGAAAGGCGGAA 5747
 QY 544 AACCGTCTATCAGGCGGATGCGCCACTACGTGAACCACTACCCCAATCAAGTTTTTTGGG 603
 DB 5746 AACCGTCTATCAGGCGGATGCGCCACTACGTGAACCACTACCCCAATCAAGTTTTTTGGG 5687
 QY 604 GTGAGGTGCGGTAAAGCACTAAATCGAAACCTTAAAGGAGCGCCCGATTTAGAGCTTG 663
 DB 5686 GTGAGGTGCGGTAAAGCACTAAATCGAAACCTTAAAGGAGCGCCCGATTTAGAGCTTG 5627
 QY 664 ACGGGAAAGCGGCGCAACGTGCGGAGAAAGGAGGAGAAAGCGGAGCGGCGC 723
 DB 5626 ACGGGAAAGCGGCGCAACGTGCGGAGAAAGGAGGAGAAAGCGGAGCGGCGC 5567
 QY 724 TAGGCGCTGCGCAAGTGTAGCGGTACAGCTGCGCGTAAACAGGAGCGGCGGCTTAA 783
 DB 5566 TAGGCGCTGCGCAAGTGTAGCGGTACAGCTGCGCGTAAACAGGAGCGGCGGCTTAA 5507
 QY 784 TGCAGCGCTACAGGCGGCTGCTACTATGGTGTCTTACAGAGCAGTATAACGTTCTCT 843
 DB 5506 TGCAGCGCTACAGGCGGCTGCTACTATGGTGTCTTACAGAGCAGTATAACGTTCTCT 5447
 QY 844 CTTGGATACAGAGCGGAGCTTAAACAGGAGCGGCGGCTTAAACAGGAGCGGCGG 903
 DB 5446 CTTGGATACAGAGCGGAGCTTAAACAGGAGCGGCGGCTTAAACAGGAGCGGCGG 5387
 QY 904 GTAGCCAGAACTCTTGAAGTGTCTTATATCATAGTGAGGCGGCGGCTTAAACAGGAG 963
 DB 5386 GTAGCCAGAACTCTTGAAGTGTCTTATATCATAGTGAGGCGGCGGCTTAAACAGGAG 5327
 QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTGTATAGTAAATACATCCTTG 1023
 DB 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTGTATAGTAAATACATCCTTG 5267
 QY 1024 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGGTAAATATCCAGAACAAATATTACGC 1083
 DB 5266 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGGTAAATATCCAGAACAAATATTACGC 5207
 QY 1084 CAGCCATTGCAACAGGAAACCGCTCATGGAATACCTACATTTTACGCTCAATCTCT 1143
 DB 5206 CAGCCATTGCAACAGGAAACCGCTCATGGAATACCTACATTTTACGCTCAATCTCT 5147
 QY 1144 GAATGATATTTTACATTTGGCAGATTCACAGTTCACAGCAGGAGTAAATAAAGGGACAT 1203
 DB 5146 GAATGATATTTTACATTTGGCAGATTCACAGTTCACAGCAGGAGTAAATAAAGGGACAT 5087
 QY 1204 TCTGGCCACACAGAG 1217
 DB 5086 TCTGGCCACACAGAG 5073

ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/995,243A
FILING DATE: 19-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/978,893
FILING DATE: 10-NOV-1992
APPLICATION NUMBER: US 08/440,787
FILING DATE: 15-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-IX 2955
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7294 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: circular
US-08-995-243A-5

Query Match 94.6%; Score 1150.8; DB 13; Length 7294;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATGTCATAGCTGTTCTCTGTTGAAATGTTATCGGCTCAACAATCCACACAACAT 123
DB 6226 ATCTGTTGTCATAGCTGTTCTCTGTTGAAATGTTATCGGCTCAACAATCCACACAACAT 6167

QY 124 ACGAGCCGGAAGCATAAAGTGTAAAGCTGGGCTGCTTCAATGAGTGAGTAACTACACAT 183
DB 6166 ACGAGCCGGAAGCATAAAGTGTAAAGCTGGGCTGCTTCAATGAGTGAGTAACTACACAT 6107

QY 184 AATTGCGTTGGCTCACTGCCGCTTCCAGTCGGGAACCTGTCGTGCCAGCTGCATTA 243
DB 6106 AATTGCGTTGGCTCACTGCCGCTTCCAGTCGGGAACCTGTCGTGCCAGCTGCATTA 6047

QY 244 ATGAATCGGCACGCGGGGAGAGCGGTTGCGTATGCGCCAGCGGTTGTTTC 303
DB 6046 ATGAATCGGCACGCGGGGAGAGCGGTTGCGTATGCGCCAGCGGTTGTTTC 5987

QY 304 TTTTCACAGTGAGACGGGCAACAGCTGATTCCTTCCAGCTGCGGCTGAGAGAGTT 363
DB 5986 TTTTCACAGTGAGACGGGCAACAGCTGATTCCTTCCAGCTGCGGCTGAGAGAGTT 5927

QY 364 GCAGCAAGCGGTCCAGCTGTTGTTGCCCCAGCAGGGAATCCTGTTGATGTTGTTTC 423
DB 5926 GCAGCAAGCGGTCCAGCTGTTGTTGCCCCAGCAGGGAATCCTGTTGATGTTGTTTC 5867

QY 424 CCAATCGCAAAATCCCTTATAAATCAAAAGATAGCCGAGATAGGTTGAGTGTGT 483
DB 5866 CCAATCGCAAAATCCCTTATAAATCAAAAGATAGCCGAGATAGGTTGAGTGTGT 5807

QY 484 TCCAGTTTGGAAACAGAGTCCACTATTAAAGACGTGGACTCCAAGTCAAAAGGGCGAAA 543
DB 5806 TCCAGTTTGGAAACAGAGTCCACTATTAAAGACGTGGACTCCAAGTCAAAAGGGCGAAA 5747

QY 544 AACCGTCTATCAGGGGGATGGCCCACTAGCTGAACCATCACCCCAATCAAGTTTTTGGG 603

Db 5746 AACCGTCTATCAGGGCGATGGCCCACTAGCTGAACCATCACCCCAATCAAGTTTTTGGG 5687

QY 604 GTCGAGGTGCGGTAAAGCACTAAATCGNACCCTAAAGGAGGCCCGGATTTAGAGCTTG 663

Db 5686 GTCGAGGTGCGGTAAAGCACTAAATCGNACCCTAAAGGAGGCCCGGATTTAGAGCTTG 5627

QY 664 ACGGGAAAGCGCGCAACAGTGGCGAGAAAGGAAGGAAAGCAAGGAGGAGCGGCGC 723

Db 5626 ACGGGAAAGCGCGCAACAGTGGCGAGAAAGGAAGGAAAGCAAGGAGGAGCGGCGC 5567

QY 724 TAGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCGCGCGCTTAA 783

Db 5566 TAGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCGCGCGCTTAA 5507

QY 784 TCGCGCGCTACAGGGCGGTACTATGTTGCTTACGAGCAGCTATTAACGTCTTCT 843

Db 5506 TCGCGCGCTACAGGGCGGTACTATGTTGCTTACGAGCAGCTATTAACGTCTTCT 5447

QY 844 CTTTGAATCAGAGCGGGAGCTAAACAGAGGCGGATTAAGGATTTTATAGACAGGACG 903

Db 5446 CTTTGAATCAGAGCGGGAGCTAAACAGAGGCGGATTAAGGATTTTATAGACAGGACG 5387

QY 904 GTACGCCAGAACTTTGAGAGTGTATTAATCACTAGGCGGAGGAGTAAAGAGTCT 963

Db 5386 GTACGCCAGAACTTTGAGAGTGTATTAATCACTAGGCGGAGGAGTAAAGAGTCT 5327

QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAATTAACATCACTTG 1023

Db 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAATTAACATCACTTG 5267

QY 1024 CCTGAGTAGAAGAACTCAAACTATCGGCTGCTGTTGTAATATCCAGAACATATTACCGC 1083

Db 5266 CCTGAGTAGAAGAACTCAAACTATCGGCTGCTGTTGTAATATCCAGAACATATTACCGC 5207

QY 1084 CAGCCATTCACAGCAAAACCTCATGGAATACCTACATTTTGACGCTCAATCTCT 1143

Db 5206 CAGCCATTCACAGCAAAACCTCATGGAATACCTACATTTTGACGCTCAATCTCT 5147

QY 1144 GAAATGGATTTTACATTTGGCAGATTCACCACTGACAGCAGGAGTAAATTAAGGGACAT 1203

Db 5146 GAAATGGATTTTACATTTGGCAGATTCACCACTGACAGCAGGAGTAAATTAAGGGACAT 5087

QY 1204 TCTGGCCACAGAG 1217

Db 5086 TCTGGCCACAGAG 5073

RESULT 14
US-09-727-311-1/c
; Sequence 1, Application US/09727311
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; TITLE OF INVENTION: RANDOMIZED PEPTIDES
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: United States
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/09/727,311
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 07/767,436
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P31 9072
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: circular
 ;
 US-09-727-311-1

Query Match 94.6%; Score 1150.8; DB 29; Length 7294;
 Best Local Similarity 99.8%; Pred. No. 0;
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 ;
 QY 64 ATCATGGTCATAGCTGTTTCTGTTGAAATGTTTATCGGCTCACAATTCACACACAAT 123
 DB 6226 ATCTGGTGCATAGCTGTTTCTGTTGAAATGTTTATCGGCTCACAATTCACACACAAT 6167
 QY 124 ACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTTAATGAGTGAAGTCACTACAT 183
 DB 6166 ACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTTAATGAGTGAAGTCACTACAT 6107
 QY 184 AATTGCGTTGCGCTACATGCGCGCTTTCCAGTCGCGGAACCTGTCGTGCCAGCTGCATTA 243
 DB 6106 AATTGCGTTGCGCTACATGCGCGCTTTCCAGTCGCGGAACCTGTCGTGCCAGCTGCATTA 6047
 QY 244 ATGAATCGGCCAACCGCGGGAGAGCGGTTTGGCTATTGGGCCCGCAGGCTGGTTTTC 303
 DB 6046 ATGAATCGGCCAACCGCGGGAGAGCGGTTTGGCTATTGGGCCCGCAGGCTGGTTTTC 5987
 QY 304 TTTTACCAGTGAACGGGCAACAGCTGATGCGCTTCCAGCTGCGGCTGGCCCTGAGAGATT 363
 DB 5986 TTTTACCAGTGAACGGGCAACAGCTGATGCGCTTCCAGCTGCGGCTGGCCCTGAGAGATT 5927
 QY 364 GCAGCAAGCGTCCAGCTGTTTGGCCCGCAGCGGCAAAATCCTGTTGATGTTGTTTC 423
 DB 5926 GCAGCAAGCGTCCAGCTGTTTGGCCCGCAGCGGCAAAATCCTGTTGATGTTGTTTC 5867
 QY 424 CGAATCGGCAAAATCCTTATAATCAAGAATAGCCCGAGATAGGTTGAGTGTGT 483
 DB 5866 CGAATCGGCAAAATCCTTATAATCAAGAATAGCCCGAGATAGGTTGAGTGTGT 5807
 QY 484 TCCAGTTTGAACAAGAGTCCACTATTAAAGAGCTGACCTCCAACTCAAGTCAAGTCAAGT 543
 DB 5806 TCCAGTTTGAACAAGAGTCCACTATTAAAGAGCTGACCTCCAACTCAAGTCAAGTCAAGT 5747
 QY 544 AACCGTCTATCAGGGCGATGCCCATACCTGTAACCATCACCACCAATCAAGTCAAGTCAAGT 603
 DB 5746 AACCGTCTATCAGGGCGATGCCCATACCTGTAACCATCACCACCAATCAAGTCAAGTCAAGT 5687
 QY 604 GTCAGGTGCGGTAAGCCTAATCGGACCTTAAGAGGAGCCCCCGATTTAGAGTTG 663
 DB 5686 GTCAGGTGCGGTAAGCCTAATCGGACCTTAAGAGGAGCCCCCGATTTAGAGTTG 5627
 QY 664 ACGGGGAAGCCGCGGAGAGTGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 723
 DB 5626 ACGGGGAAGCCGCGGAGAGTGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5567
 QY 724 TAGGGGCTGGCAAGTGTAGCGGTGACGCTGCGGTAAACCAACCAACCAACCAACCAACCAAC 783
 DB 5566 TAGGGGCTGGCAAGTGTAGCGGTGACGCTGCGGTAAACCAACCAACCAACCAACCAACCAAC 5507
 QY 784 TGGCGCGCTACAGGCGCGTACATGTTGCTGTTGAGCAGCAGTATAACGTTGCTTTCCT 843
 DB 5506 TGGCGCGCTACAGGCGCGTACATGTTGCTGTTGAGCAGCAGTATAACGTTGCTTTCCT 5447

QY 844 CGTTGGATCAGACCGGGAGCTAAACAGGAGGCGGATTAAGGGGATTTTAGACAGGAACG 903
 DB 5446 CGTTGGATCAGACCGGGAGCTAAACAGGAGGCGGATTAAGGGGATTTTAGACAGGAACG 5387
 QY 904 GTACGCCAGAACTCTTGAGAAAGTGTATTAATCAGTGAGGCCACCGAGTAAAGAGTCT 963
 DB 5386 GTACGCCAGAACTCTTGAGAAAGTGTATTAATCAGTGAGGCCACCGAGTAAAGAGTCT 5327
 QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTAAATCAATCACTTTG 1023
 DB 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTAAATCAATCACTTTG 5267
 QY 1024 CTTGAGTAGAAGAACTCAAACTATCGCCTTGGTGGTAAATATCCAGAACATATACCGC 1083
 DB 5266 CTTGAGTAGAAGAACTCAAACTATCGCCTTGGTGGTAAATATCCAGAACATATACCGC 5207
 QY 1084 CAGCCATTGCAACAGGAAACGCTCATGGAATACCTACATTTTGACGCTCAATCTCT 1143
 DB 5206 CAGCCATTGCAACAGGAAACGCTCATGGAATACCTACATTTTGACGCTCAATCTCT 5147
 QY 1144 GAATCGATTATTTACATTGGCAGATTCCAGCTGACACGACGAGTAAATAAAGGGACAT 1203
 DB 5146 GAATCGATTATTTACATTGGCAGATTCCAGCTGACACGACGAGTAAATAAAGGGACAT 5087
 QY 1204 TCTGGCCAAACAGAG 1217
 DB 5086 TCTGGCCAAACAGAG 5073
 RESULT 15
 US-09-727-311-5/c
 ; Sequence 5, Application US/09727311
 ; GENERAL INFORMATION:
 ; APPLICANT: Huse, William D.
 ; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
 ; TITLE OF INVENTION: RANDOMIZED PEPTIDES
 ; NUMBER OF SEQUENCES: 61
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Pretty, Schroeder, Brueggemann & Clark
 ; STREET: 444 South Flower Street, Suite 2000
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: United States
 ; ZIP: 90071
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/727,311
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/767,436
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Campbell, Cathryn A
 ; REGISTRATION NUMBER: 31,815
 ; REFERENCE/DOCKET NUMBER: P31 9072
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619) 535-9001
 ; TELEFAX: (619) 535-8949
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 7294 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: both
 ; TOPOLOGY: circular
 ;
 US-09-727-311-5

Query Match									
Best Local Similarity 94.6%; Score 1150.8; DB 29; Length 7294;									
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
Qy	64	ATCATGTGATAGTCTTTCTCTGTGTGAAATTTGTTATCCCGTCCACAAATTCACACAAACAT	123						
Db	6226	ATCTGTGTCATAGTCTTTCTCTGTGTGAAATTTGTTATCCCGTCCACAAATTCACACAAACAT	6167						
Qy	124	ACGAGCCGGAAGCAATAAAGCTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTAACTCAACAT	183						
Db	6166	ACGAGCCGGAAGCAATAAAGCTGTAAAGCTGGGGTGCCTTAATGAGTGAGCTAACTCAACAT	6107						
Qy	184	AATGTGCTTGGCTCACTGCCGCTTCCAGTCGGGAAACCTGTCGTCGCCAGCTGCATT	243						
Db	6106	AATGTGCTTGGCTCACTGCCGCTTCCAGTCGGGAAACCTGTCGTCGCCAGCTGCATT	6047						
Qy	244	ATGAATCGGCAACGCGGGGAGAGCGGTTTGCCTATTTGGGCGCCAGGGTGTTTTC	303						
Db	6046	ATGAATCGGCAACGCGGGGAGAGCGGTTTGCCTATTTGGGCGCCAGGGTGTTTTC	5987						
Qy	304	TTTTTCACAGTGAGACGGGCAACAGCTGATTGCCCTTCACCGCTGGGCCCTGAGAGCTT	363						
Db	5986	TTTTTCACAGTGAGACGGGCAACAGCTGATTGCCCTTCACCGCTGGGCCCTGAGAGCTT	5927						
Qy	364	GCAGCAAGCGGTCCACGCTGCTTTGCCCGACGAGCGAAATCCCTGTTTGATGTGGTTC	423						
Db	5926	GCAGCAAGCGGTCCACGCTGCTTTGCCCGACGAGCGAAATCCCTGTTTGATGTGGTTC	5867						
Qy	424	CGAAATCGGCAAAATCCCTTATAATCAAAAGATPAGCCGAGATPAGGTTGAGTGTGT	483						
Db	5866	CGAAATCGGCAAAATCCCTTATAATCAAAAGATPAGCCGAGATPAGGTTGAGTGTGT	5807						
Qy	484	TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACTGGACTCCACGTCACAAAGGGCGAA	543						
Db	5806	TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACTGGACTCCACGTCACAAAGGGCGAA	5747						
Qy	544	AACGCTCTATCAGGGCGATGCGCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGGG	603						
Db	5746	AACGCTCTATCAGGGCGATGCGCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGGG	5687						
Qy	604	GTGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAGGGAGCCCGCGATTTAGAGCTTG	663						
Db	5686	GTGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAGGGAGCCCGCGATTTAGAGCTTG	5627						
Qy	664	ACGGGAAGCGCGGAGAGTGGCGGAGAAAGGAGGAAAGCGAAAGGAGCGGGCGC	723						
Db	5626	ACGGGAAGCGCGGAGAGTGGCGGAGAAAGGAGGAAAGGAGGAGCGGGCGC	5567						
Qy	724	TAGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACACCGCCGCGCTTAA	783						
Db	5566	TAGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACACCGCCGCGCTTAA	5507						
Qy	784	TGCGCGCTACAGGGCGGTACTATGTTGCTTTGACGAGCAGGTATACGTCTTTCCT	843						
Db	5506	TGCGCGCTACAGGGCGGTACTATGTTGCTTTGACGAGCAGGTATACGTCTTTCCT	5447						
Qy	844	CGTTGGAATCAGAGCGGGAGCTAAACAGGAGCCCGGATTAAGGGATTTTAGACAGGAACG	903						
Db	5446	CGTTGGAATCAGAGCGGGAGCTAAACAGGAGCCCGGATTAAGGGATTTTAGACAGGAACG	5387						
Qy	904	GTACGCCAGAACTTTGAGAGTGTTTTATAATCACTAGAGGCCACCGAGTAAAGAGTCT	963						
Db	5386	GTACGCCAGAACTTTGAGAGTGTTTTATAATCACTAGAGGCCACCGAGTAAAGAGTCT	5327						
Qy	964	GTCCATACGCCAAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAATAACATCACTTG	1023						
Db	5326	GTCCATACGCCAAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAATAACATCACTTG	5267						
Qy	1024	CTGTAGTAGAAGAACTCAAACTATCGGCTTGTGTGTAATATCCAGAACTATTACCGC	1083						
Db	5266	CTGTAGTAGAAGAACTCAAACTATCGGCTTGTGTGTAATATCCAGAACTATTACCGC	5207						
Qy	1084	CAGCCATTGCAACAGGAAACCGCTCATGGAAATACCTACATTTTGACGCTCAATCGTCT	1143						

Search completed: August 1, 2002, 10:59:18
Job time: 11349 sec

Db	5206	CAGCCATTGCAACAGGAAACCGCTCATGGAATACTTACATTTTGACGCTCAATCGTCT	5147
Qy	1144	GAATGGATTATTTACATTTGGCAGATTCCACGAGTCCACAGGACCAAGTAATAAAGGACAT	1203
Db	5146	GAATGGATTATTTACATTTGGCAGATTCCACGAGTCCACAGGACCAAGTAATAAAGGACAT	5087
Qy	1204	TCTGGCCCAACAGAG	1217
Db	5086	TCTGGCCCAACAGAG	5073

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 08:40:05 ; Search time 348.01 Seconds
(without alignments)
7578.543 Million cell updates/sec

Title: US-10-014-743-1
Perfect score: 1217
Sequence: 1 GCCAGCTTCATCCTGCA.....GGACATTCGCGCAACAGAG 1217

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 1353370 seqs, 1083569762 residues

Total number of hits satisfying chosen parameters: 2706740

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_NA_New.*

- 1: /cgn2_6/ptodata/1/pna/PCT_NEW_COMB.seq.*
- 2: /cgn2_6/ptodata/1/pna/US05_NEW_COMB.seq.*
- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
- 4: /cgn2_6/ptodata/1/pna/US08_NEW_COMB.seq.*
- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	931.2	76.5	9532	1	PCT-US02-12405-451
C 2	931.2	76.5	9532	7	US-10-045-674-451
C 3	928	76.3	10251	1	PCT-US02-12405-582
C 4	928	76.3	10251	7	US-10-045-674-582
5	592.6	48.7	605	5	US-09-334-818A-4
6	592.6	48.7	605	5	US-09-334-818A-23
7	590.4	48.5	601	5	US-09-334-818A-19
8	591	47.7	604	5	US-09-334-818A-24
9	577.4	47.4	605	5	US-09-334-818A-17
10	574.4	47.2	605	5	US-09-334-818A-12
11	574	47.2	598	5	US-09-334-818A-11
12	572.4	47.0	602	5	US-09-334-818A-22
13	564	46.3	601	5	US-09-334-818A-18
14	558.8	45.9	595	5	US-09-334-818A-5
15	551.4	45.3	605	5	US-09-334-818A-21
16	551	45.3	596	5	US-09-334-818A-13
17	551	45.3	597	5	US-09-334-818A-10
18	526.6	43.3	599	5	US-09-334-818A-6
19	505.8	41.6	591	5	US-09-334-818A-3
20	488	40.1	619	5	US-09-334-818A-20
21	459.8	37.8	597	5	US-09-334-818A-16
22	445.2	36.6	602	5	US-09-334-818A-14
C 23	432.4	35.5	4455	7	US-10-047-542-13
C 24	432.4	35.5	6602	7	US-10-047-542-100
25	432.4	35.5	7129	7	US-10-047-542-101

Sequence 14, Appl
Sequence 7, Appl
Sequence 522, App
Sequence 522, App
Sequence 1, Appl
Sequence 53, Appl
Sequence 70, Appl
Sequence 71, Appl
Sequence 75, Appl
Sequence 9, Appl
Sequence 46, Appl
Sequence 1, Appl
Sequence 4, Appl
Sequence 16, Appl
Sequence 32, Appl
Sequence 40, Appl
Sequence 34, Appl
Sequence 37, Appl
Sequence 35, Appl

26 432.4 35.5 8074 7 US-10-047-542-14
27 426 35.0 585 5 US-09-334-818A-7
28 399.4 32.8 6880 1 PCT-US02-12405-522
29 399.4 32.8 6880 7 US-10-045-674-522
C 30 399 32.8 4026 5 US-09-949-039-1
C 31 399 32.8 10325 7 US-10-112-267-53
32 395.2 32.5 602 5 US-09-334-818A-15
33 381.2 31.3 8157 7 US-10-038-722-70
34 381.2 31.3 8584 7 US-10-038-722-71
35 381.2 31.3 8590 7 US-10-038-722-75
C 36 379.6 31.2 652 5 US-09-370-582C-9
37 379.6 31.2 2989 7 US-10-149-736-46
C 38 379.6 31.2 4570 7 US-10-049-404-1
39 379.6 31.2 4704 5 US-09-932-328-4
40 379.6 31.2 4727 5 US-09-756-577-16
C 41 379.6 31.2 4773 5 US-09-991-209-32
C 42 379.6 31.2 4847 5 US-09-756-577-40
C 43 379.6 31.2 4950 5 US-09-991-209-34
C 44 379.6 31.2 4965 5 US-09-991-209-37
C 45 379.6 31.2 4974 5 US-09-991-209-35

ALIGNMENTS

RESULT 1
PCT-US02-12405-451/c
Sequence 451, Application PC/TUS0212405

GENERAL INFORMATION:
APPLICANT: LADNER, ROBERT C.
APPLICANT: COHEN, EDWARD H.
APPLICANT: NASTRI, HORACIO G.
APPLICANT: ROOKEY, KRISTIN L.
APPLICANT: HOET, RENE
APPLICANT: HOOGENBOOM, HENDRICUS R. J. M.
TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
TITLE OF INVENTION: LIBRARIES
FILE REFERENCE: DYAX/002 CIP2
CURRENT APPLICATION NUMBER: PCT/US02/12405
CURRENT FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: 06/198,069
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: 09/837,306
PRIOR FILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 635
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 451
LENGTH: 9532
TYPE: DNA
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: MALIA3 nucleotide
OTHER INFORMATION: sequence
FEATURE:
NAME/KEY: CDS
LOCATION: (1579)..(1638)
FEATURE:
NAME/KEY: CDS
LOCATION: (2343)..(3443)
FEATURE:
NAME/KEY: CDS
LOCATION: (3945)..(4400)
FEATURE:
NAME/KEY: CDS
LOCATION: (4406)..(4450)
FEATURE:
NAME/KEY: CDS
LOCATION: (4746)..(5789)
PCT-US02-12405-451

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RESULT 2
US-10-045-674-451/c
; Sequence 451, Application US/10045674
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROOKEY, KRISTIN L.
; APPLICANT: HOET, RENE
; APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: DYAX/002 CIP2
; CURRENT APPLICATION NUMBER: US/10/045,674
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 09/837,306
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 635
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 451
; LENGTH: 9532
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: MALIA3 nucleotide
; OTHER INFORMATION: sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1579)..(1638)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2343)..(3443)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3945)..(4400)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4406)..(4450)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (4746)..(5789)
;
US-10-045-674-451

Query Match 76.5%; Score 931.2; DB 7; Length 9532;
Best Local Similarity 97.6%; Pred. No. 3.3e-256;
Matches 945; Conservative 0; Mismatches 23; Indels 0; Gaps 0;

QY 250 CGGCCAACGCGCGGGGAGAGCGGTTTGCCTATTGGGCGCCAGCGTGTTTTCTTTTCA 309
   || || || || || || || || || || || || || || || || || || || || ||
Db 7591 CGCACATTTCCCCGAAAGTGCCACCTGCAAGCTTGGATCCAGGGTGTTTTCTTTTCA 7532

QY 310 CCAGTGAGAGCGGGAACAGCTGATGCGCTTTCACGCGCTGGCCCTGAGAGAGTTGCAGCA 369
   || || || || || || || || || || || || || || || || || || || || ||
Db 7531 CCAGTGAGAGCGGCAACAGCTGATGCGCTTTCACGCGCTGGCCCTGAGAGAGTTGCAGCA 7472

QY 370 AGCGGTCCACGCTGTTGGTCCGACAGCGGCAAAATCCTGTTGATGGTGTCCGAAT 429
   || || || || || || || || || || || || || || || || || || || || ||
Db 7471 AGCGGTCCACGCTGTTGGTCCGACAGCGGCAAAATCCTGTTGATGGTGTCCGAAT 7412

QY 430 CGGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGTGTTCCAGT 489
   || || || || || || || || || || || || || || || || || || || || ||
Db 7411 CGGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGTGTTCCAGT 7352

QY 490 TTGGAACAAGAGTCCACTATTAAAGACGTGGACTCCAACGTCAAAGGGCGAAACCGT 549
   || || || || || || || || || || || || || || || || || || || || ||
Db 7351 TTGGAACAAGAGTCCACTATTAAAGACGTGGACTCCAACGTCAAAGGGCGAAACCGT 7292

QY 550 CTATCAGGCGGATGGGCCCACTAGCTGAACCATCATCCCAAAATCAAGTTTTTTTGGGGTCCGAG 609

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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CIRA05
; OTHER INFORMATION: nucleotide sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1578)..(1916)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2388)..(2843)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2849)..(2893)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3189)..(4232)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7418)..(8119)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (8160)..(9452)
; PCT-US02-12405-582
;
; Query Match 76.3% Score 928; DB 1; Length 10251;
; Best Local Similarity 97.4%; Pred. No. 2.8e-255;
; Matches 943; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
;
; QY 250 CGGCCAACGGCGGGGAGAGCGGTTTTCGTTATTTGGGCGCCAGGCTGTTTCTTTTCA 309
; DB 6034 CGCACATTTCCCGGAAAGTGCACCTGCAAGCTTGGATCCAGGCTGTTTCTTTTCA 5975
; QY 310 CCAGTGAGAGCGGGCAACAGCTGATTGCCCTTACCGCTTGGCCCTGAGAGAGTTGCAGCA 369
; DB 5974 CCAGTGAGAGCGGGCAACAGCTGATTGCCCTTACCGCTTGGCCCTGAGAGAGTTGCAGCA 5915
; QY 370 AGCGGTCCACGCTGTTTGGCCCGAGAGCGGCAAAATCTGTGTGATGGTGGTCCGAAAT 429
; DB 5914 AGCGGTCCACGCTGTTTGGCCCGAGAGCGGCAAAATCTGTGTGATGGTGGTCCGAAAT 5855
; QY 430 CGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGGTGTGTTGTTCCAGT 489
; DB 5854 CGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGGTGTGTTGTTCCAGT 5795
; QY 490 TTGGAACAAGAGTCCACATTTAAAGACGTGACCTCCACGTCNAAGGCGGAAACCGT 549
; DB 5794 TTGGAACAAGAGTCCACATTTAAAGACGTGACCTCCACGTCNAAGGCGGAAACCGT 5735
; QY 550 CTATCAGGGCGATGGCCGCTACGTGAACCATCACCCAAATCAAGTCTTTTGGGTCGAG 609
; DB 5734 CTATCAGGGCGATGGCCGCTACGTGAACCATCACCCAAATCAAGTCTTTTGGGTCGAG 5675
; QY 610 GTGCCGTAAAGCACTAAATCGGAACCTTAAAGGAGAGCCCGCCGATTTAGAGCTTGACGGG 669
; DB 5674 GTGCCGTAAAGCACTAAATCGGAACCTTAAAGGAGAGCCCGCCGATTTAGAGCTTGACGGG 5615
; QY 670 AAAGCCGCGAAGCTGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 729
; DB 5614 AAAGCCGCGAAGCTGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5555
; QY 730 GCTGCAAGTGTAGCGGTACCGTCAACACACACACACACACACACACACACACACACAC 789
; DB 5554 GCTGCAAGTGTAGCGGTACCGTCAACACACACACACACACACACACACACACACACAC 5495
; QY 790 GCTACAGGCGCGTACTATGTTGTTGACGAGCAGCTATACGCTTCTCTCTCTCTCTCT 849
; DB 5494 GCTACAGGCGCGTACTATGTTGTTGACGAGCAGCTATACGCTTCTCTCTCTCTCTCT 5435
; QY 850 AATCAGAGCGGAGCTAAACAGGAGGCGGCTTAAAGGGATTTTAGACAGGAGGAGGAGG 909
; DB 5434 AATCAGAGCGGAGCTAAACAGGAGGCGGCTTAAAGGGATTTTAGACAGGAGGAGGAGG 5375

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RESULT . 3

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; PCT-US02-12405-582/c
; Sequence 582. Application PC/TUS0212405
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROONEY, KRISTIN L.
; APPLICANT: HOET, RENE
; APPLICANT: HOOGENDOORN, HENDRICUS R. J. M.
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: DYAX/002 CIP2
; CURRENT APPLICATION NUMBER: PCT/US02/12405
; CURRENT FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: 06/198,069
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 09/837,306
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 635
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 582
; LENGTH: 10251

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QY 910 CAGAACTTGAGAACTGTTTATATATAGTGGAGCCACCGAGTAAAGAGTCTGTCCAT 969
Db 5374 CAGAACTTGAGAACTGTTTATATATAGTGGAGCCACCGAGTAAAGAGTCTGTCCAT 5315
QY 970 CACGCAAAATTAACCGTGTGAGCAATACCTTTGATTAGTAAATACATCACTTGCCTGAG 1029
Db 5314 CACGCAAAATTAACCGTGTGAGCAATACCTTTGATTAGTAAATACATCACTTGCCTGAG 5255
QY 1030 TAGAAGAACTCAAACTATCGGCTTGCTGTAATATCCAGAACTAATATACCGCCAGCCA 1089
Db 5254 TAGAAGAACTCAAACTATCGGCTTGCTGTAATATCCAGAACTAATATACCGCCAGCCA 5195
QY 1090 TTGCAACAGGAAACCGCTCATGGAATACCTTACATTTTACGCTCAATCGTCTGAATG 1149
Db 5194 TTGCAACAGGAAACCGCTCATGGAATACCTTACATTTTACGCTCAATCGTCTGAATG 5135
QY 1150 GATTATTTACATTTGCGAGATTCACGAGTCAACAGCCAGTAAATAAAGGACATTTCTGGC 1209
Db 5134 GATTATTTACATTTGCGAGATTCACGAGTCAACAGCCAGTAAATAAAGGACATTTCTGGC 5075
QY 1210 CAACAGAG 1217
Db 5074 CAACAGAG 5067

RESULT 4
US-10-045-674-582/c
; Sequence 582, Application US/10045674
; GENERAL INFORMATION:
; APPLICANT: LADNER, ROBERT C.
; APPLICANT: COHEN, EDWARD H.
; APPLICANT: NASTRI, HORACIO G.
; APPLICANT: ROONEY, KRISTIN L.
; APPLICANT: HOET, RENE
; APPLICANT: HOENBOOM, HENDRICUS R. J. M.
; TITLE OF INVENTION: NOVEL METHODS OF CONSTRUCTING LIBRARIES COMPRISING
; TITLE OF INVENTION: DISPLAYED AND/OR EXPRESSED MEMBERS OF A DIVERSE FAMILY
; TITLE OF INVENTION: OF PEPTIDES, POLYPEPTIDES OR PROTEINS AND THE NOVEL
; TITLE OF INVENTION: LIBRARIES
; FILE REFERENCE: DYAX/002 CIP2
; CURRENT APPLICATION NUMBER: US/10/045.674
; CURRENT FILING DATE: 2001-10-25
; PRIOR APPLICATION NUMBER: 60/198,069
; PRIOR FILING DATE: 2000-04-17
; PRIOR APPLICATION NUMBER: 05/837,306
; PRIOR FILING DATE: 2001-04-17
; NUMBER OF SEQ ID NOS: 635
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 582
; LENGTH: 10251
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: CJRA05
; OTHER INFORMATION: nucleotide sequence
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1578)..(1916)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2388)..(2843)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (2849)..(2893)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (3189)..(4232)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7418)..(8119)
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: (8160)..(9452)
us-10-045-674-582
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Query Match 76.3%; Score 928; DB 7; Length 10251;
Best Local Similarity 97.4%; Pred. No. 2.8e-255;
Matches 943; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
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QY 250 CGGCCAACCGCGGGGAGAGCGGTTTGGCGCGCCAGGGTGGTTCCTTTTCCTTTCA 309
Db 6034 CGCACATTTCCCGAANAAGTCCACCTGCAAGCTTGGATCCAGGTGGTTCCTTTCA 5975
QY 310 CCAAGTGAGACGGGCAACAGCTGATTCCTTCCACCGCTTGGCCCTGAGAGAGTTCGACCA 369
Db 5974 CCAGTGAGACGGGCAACAGCTGATTCCTTCCACCGCTTGGCCCTGAGAGAGTTCGACCA 5915
QY 370 AGCGGTCCACGCTGGTTTGGCCCGCAGGCGAANAATCCTTTGTGATGGTGGTTCGGAAT 429
Db 5914 AGCGGTCCACGCTGGTTTGGCCCGCAGGCGAANAATCCTTTGTGATGGTGGTTCGGAAT 5855
QY 430 CGGCAAAATCCCTTATATAATCAAAAGAAATAGCCCGAGATAGGTTGAGTTGTTCCAGT 489
Db 5854 CGGCAAAATCCCTTATATAATCAAAAGAAATAGCCCGAGATAGGTTGAGTTGTTCCAGT 5795
QY 490 TTGGAAACAGAGTCCACTATTAAGAAACGCTGGACTCCAACGTCAAAGGGCGAANAACCGT 549
Db 5794 TTGGAAACAGAGTCCACTATTAAGAAACGCTGGACTCCAACGTCAAAGGGCGAANAACCGT 5735
QY 550 CTATCAGGGCGATGGCCCACTAGTGAACCATCACCAATCAAGTTTTTGGGGTGCAG 609
Db 5734 CTATCAGGGCGATGGCCCACTAGTGAACCATCACCAATCAAGTTTTTGGGGTGCAG 5675
QY 610 GTGCCGTAAAGCACCTAAATCGGAACCCCTAAAGGGAGCCCGCGATTTAGAGCTTCACGGGG 669
Db 5674 GTGCCGTAAAGCACCTAAATCGGAACCCCTAAAGGGAGCCCGCGATTTAGAGCTTCACGGGG 5615
QY 670 AAAGCCGCGAAGCTGGCGAGAAAGAAAGGAGGAAAGGAGGAGGAGGAGGAGGAGGAGG 729
Db 5614 AAAGCCGCGAAGCTGGCGAGAAAGGAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 5555
QY 730 GCTGCAAGTGTAGCGGTACGCTGCGGTAAACACACACCGCCGCTTAATCGGCC 789
Db 5554 GCTGCAAGTGTAGCGGTACGCTGCGGTAAACACACACCGCCGCTTAATCGGCC 5495
QY 790 GCTACAGGGCGCTACTATGTTGCTTTGACGAGCAGCTATACGTCGTTTCCTCGTTGG 849
Db 5494 GCTACAGGGCGCTACTATGTTGCTTTGACGAGCAGCTATACGTCGTTTCCTCGTTGG 5435
QY 850 AATCAGACCGGGAGCTAAACAGGAGGCGGATTAAGGGGATTTTAGACAGAAACGGTACGC 909
Db 5434 AATCAGACCGGGAGCTAAACAGGAGGCGGATTAAGGGGATTTTAGACAGAAACGGTACGC 5375
QY 910 CAGAACTTGAGAACTGTTTATATATAGTGGAGCCACCGAGTAAAGAGTCTGTCCAT 969
Db 5374 CAGAACTTGAGAACTGTTTATATATAGTGGAGCCACCGAGTAAAGAGTCTGTCCAT 5315
QY 970 CACGCAAAATTAACCGTGTGAGCAATACCTTTGATTAGTAAATACATCACTTGCCTGAG 1029
Db 5314 CACGCAAAATTAACCGTGTGAGCAATACCTTTGATTAGTAAATACATCACTTGCCTGAG 5255
QY 1030 TAGAAGAACTCAAACTATCGGCTTGCTGTAATATCCAGAACTAATATACCGCCAGCCA 1089
Db 5254 TAGAAGAACTCAAACTATCGGCTTGCTGTAATATCCAGAACTAATATACCGCCAGCCA 5195
QY 1090 TTGCAACAGGAAACCGCTCATGGAATACCTTACATTTTACGCTCAATCGTCTGAATG 1149
Db 5194 TTGCAACAGGAAACCGCTCATGGAATACCTTACATTTTACGCTCAATCGTCTGAATG 5135
QY 1150 GATTATTTACATTTGCGAGATTCACGAGTCAACAGCCAGTAAATAAAGGACATTTCTGGC 1209
Db 5134 GATTATTTACATTTGCGAGATTCACGAGTCAACAGCCAGTAAATAAAGGACATTTCTGGC 5075
QY 1210 CAACAGAG 1217
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492 tgttcagtttggacaagantccactatttaaagaacgtggactccaacgtccaaagggcg 551
DB
541 ARAAACCTCTTATCAGGGCGATGGCCCATAGCTGAACCATCACCCAATCAAG 594
QY
552 aaaaacnctctatcagggcgatggccactcagctgaaccatcacccaatcaas 605
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RESULT      6
US-09-334-818A-23
> Sequence 23, Application US/09334818A
> GENERAL INFORMATION:
>
> APPLICANT: DAVIS, MARIA
> APPLICANT: FULLER, CARL W.
> APPLICANT: MAMONE, JOSEPH A.
>
> APPLICANT: HUANG, LIN
>
> TITLE OF INVENTION: FY7 POLYMERASE
> FILE REFERENCE: PB9817
> CURRENT APPLICATION NUMBER: US/09/334,818A
> CURRENT FILING DATE: 1999-06-17
> PRIOR APPLICATION NUMBER: 60/089,556
> PRIOR FILING DATE: 1998-06-17
> NUMBER OF SEQ ID NOS: 27
> SOFTWARE: PatentIn Ver. 2.1
>
> SEQ ID NO 23
>
> LENGTH: 605
>
> TYPE: DNA
>
> ORGANISM: Thermus sp.
>
> FEATURE:
>
> NAME/KEY: modified_base
>
> LOCATION: (1)
>
> OTHER INFORMATION: a, t, c or g
>
> FEATURE:
>
> NAME/KEY: modified_base
>
> LOCATION: (512)
>
> OTHER INFORMATION: a, t, c or g
>
> US-09-334-818A-23

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Query Match	48.7%	Score 592.6	DB 5	Length 605
Best Local Similarity	99.7%	Pred. No. 1.3e-159		
Matches 592	Conservative	1	Mismatches	1
			Indels	0
			Gaps	0
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12	gccaagcttgcatgctgcagctcgactctagagatcccggtaccgagctcgaaattc	71		
61	GTAATCATGGTCAATAGCTCTTTCCCTGTGCAATCTTATCCGCTCACAAATTCACACAA	120		
72	gtaatcatggtcatagctgtttccctgtggaatgtctatccgctcaaatctccacaaa	131		
121	CATACGAGCGCGAAGCATAAAGTGTAAAGCCTGGGTGCGCTAATGAGTGAGCTTAACTCAC	180		
132	catacgagcgcggaagcataaagtgtaaaacctgggtgcctaatagtgagctaactcac	191		
181	ATTAATGGTGTGCGCTCACTGCCCGCTTTCAGTCTGGGAAACCTGTCTGCCACAGCTGCA	240		
192	attaattggtgtgcgtcactgcgccgcttcccgctgaggaaacctgtctgtccagctgca	251		
241	TTAATCAATCGCGCAACGCGCGGGAGAGCGGTTTCGGCTATTGGGGCGCCAGGTGGTTT	300		
252	ttaatgaaatcgccaaacgcgcgaggagagcggttgcgtattggcgccagggttggttt	311		
301	TTCTTTTACCACTGACACGGGCACACAGCTGATTGCCCTTCACCGCTGGCGCTTGAGAGA	360		
312	ttcttttcaacagtgagacgaggcaacagctgtattgccccctcaacgcctggccctgagaga	371		
361	GTTTCAGCAAGCGGTCACAGCTGTGTTTCCGCCAGCAGCGGAAATTCCTGTTTGATGGTG	420		
372	gttgcaagaacggttccacgctggttggccccagcaggcgaaatctgtttgattgagtggtg	431		
421	TTCCGGAATCGCGAAAATCCCTTTAATCAAAAGAATAGCCCGAGATAGGTTTGAGTGT	480		
432	ttcggaatcggcgaaatcccttataatcaaaagaaatagcccagatagaggttgagtgat	491		

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Db      5074 CAACAGG 5067
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RESULT      5
US-09-334-818A-4
; Sequence 4, Application US/09334818A
; GENERAL INFORMATION:
; APPLICANT: DAVIS, MARIA
; APPLICANT: FULLER, CARL W.
; APPLICANT: MAMONE, JOSEPH A.
; APPLICANT: HUANG, LIN
; TITLE OF INVENTION: FY7 POLYMERASE
; FILE REFERENCE: PB9817
; CURRENT APPLICATION NUMBER: US/09/334,818A
; CURRENT FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/089,556
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 605
; TYPE: DNA
; ORGANISM: Thermus sp.
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (512)
; OTHER INFORMATION: a, t, c or g
;
US-09-334-818A-4

Query Match      48.7%; Score 592.6; DB 5; Length 605;
Best Local Similarity 99.7%; Pred. No. 1.3e-159;
Matches 592; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 GCCAAGCTTGATGCCCTGACGTCACGCTAGAGATCCCGGGTACCAGCTCGAATTC 60
Db 12 gccagcttgatgctgcagtgacgtcctgagagatccccgggtacgagctcgaaattc 71
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QY 61 GTAATCATGGTTCATAGCTGTTTCCTGTGTGAATGTGTATCCGCTCACAATTCACACAA 120
Db 72 gtaacatggtcatagctgatttcctgctgtgaaattgttatccgtcacaaattccacaaa 131
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QY 121 CATACGAGCGGAAGCATAAGCTAAGAGCTGAGCTGGGTCCTTAATGAGTGAGTAACTCAC 180
Db 132 catcacgagcggaagcataaagtgtaaagcctgggggtccctaaagagtgagctaaactcac 191
|||||
QY 181 ATTAATGGGTGGCTGCTCACTCCCGCTTTCCAGTCGGGAAACCTGTGCTGCCAGCTGCA 240
Db 192 ataatgcgttgctgctcaactgccgcgttccagtcgggaaacctgctgccccagctgca 251
|||||
QY 241 TTAATGAATGGCCAAACGCGCGGGAGAGCGCGTTTGCCTATTGGCGCCAGGGTGGTTT 300
Db 252 ttaatgaatcgccaaacgcgcggggagagcgaggtttgcgtatctggggcgcagggttggtt 311
|||||
QY 301 TTCCTTTTACCAGTGAGAGCGGCAACAGCTGATTGCCCTTTCACCGCTCGCCCTGAGAGA 360
Db 312 tctctttccaccagttagacgagcgcaacagctgattgcccttaccgcctggccctgagaga 371
|||||
QY 361 GTTGCAGCAAGCGGTCACGCTGGTTTGGCCCGAGCAGCGGAATAATCCTGTTGATCGTGG 420
Db 372 gttgcagcaagcgggtccacgctggtttgccccagcaggcgaaatccctgttgatggtggt 431
|||||
QY 421 TTCGGAATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGT 480
Db 432 ttcggaatcggcaaaatcccttataaatacaaaagaatagcccgagataggggtgagtggt 491
|||||
QY 481 TGTTCCTCAGTTTGGAAACAGAGTCCACTATTAAACAGCTGAGCTCCCAAGCTCAAGGGCG 540
Db 491 tgttcctcagtttggaaacagagtgccactatttaaacagctgagctcccaagctcaagggcg 540
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RESULT      7
US-09-334-818A-19
; Sequence 19, Application US/09334818A
; GENERAL INFORMATION:
; APPLICANT: DAVIS, MARIA
; APPLICANT: FULLER, CARL W.
; APPLICANT: MAMONE, JOSEPH A.
; APPLICANT: HUANG, LIN
; TITLE OF INVENTION: FV7 POLYMERASE
; FILE REFERENCE: PB9817
; CURRENT APPLICATION NUMBER: US/09/334,818A
; CURRENT FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/089,556
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Thermus sp.
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (2)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (580)
; OTHER INFORMATION: a, t, c or g
US-09-334-818A-19

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Query Match	47.7%	Score 581;	DB 5;	Length 604;	
Best Local Similarity	99.7%;	Pred. No. 2.8e-156;			
Matches 592;	Conservative 0;	Mismatches 1;	Indels 1;	Gaps 1;	
QY 1	GCCAAAGCTTCATGCTGCTGAGGTCGACCTCTAGAGGATCCCGGGTATCCGAGCTCGAATTC	60			
Db					
QY 12	gccaaagcttgcatgctgctgagctgagctctagagatcccggttacccagctcgaattc	71			
Db					
QY 61	gpaatcatggctcatagctgtttctctgtctgtaaatgtttatccggtcacaattccacacaa	120			
Db					
QY 72	gtaatatggctcatagctgtttctctgtgtaaatgtttatccggtcacaattccacacaa	131			
Db					
QY 121	CATACGAGCCGGAGAGCATAAAGTGTAAAGCTCGGGTGCCTTAATGAGTGAGCTAACTCAC	180			
Db					
QY 132	catacgagccgggaagca caaagtgtaaaagctgggggtgcctaaTlgaTgagctaaactcac	191			
Db					
QY 191	ATTAAATTCGCTTGCGCTCACTGCCCGCTTTCACAGTCGGGAAACCTGTCGTGCCAGCTGCA	240			
Db					
QY 192	attaattgcgttgctctcaactgccgcgtttccagtcgggaaacctgcgtgcagcgcgca	251			
Db					
QY 241	TTAATGAATCGGCCCAACGCGGGGAGAGCGGTTTCGGTATTGGGGCCACGGGTGGTTT	300			
Db					
QY 252	ttaatgaatcgcccaacgcgcg9999aagcgggttgctgattgggcgcaggggtggtt	311			
Db					
QY 301	TTCTTTTCACAGTGAACGCGGCAACAGCTGATTGCCCTTTCACCGCTGGCCCTTGAGAGA	360			
Db					
QY 312	tctctttccacagtgagacgggcaacagctgattgccttccacgcctgagcctgagaga	371			
Db					
QY 361	GTTGCAGCAAGCGTCCACGCTGGTTTGGCCCCAGCAGCGGAAATCCTGTTTGATGGTGG	420			
Db					
QY 372	gttgcagcaagcgggtccacgctggtttgccccagcaggcgaaatcctgtttgatcgggtgg	431			
Db					
QY 421	TTCCGAAATCGCGAAATCCCTTATTAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGT	480			
Db					

QY	121	CATACGAGCCGGAAGCATAAAGTGTAAAGCCTGGGGTGCCTAATCAGTCAGTCAACTACAC	180
Db	132	catacgagcgggaagcataaagtgtaaaagctggctctaaagtagagtaactaacac	191
QY	181	ATTAATTTGCGTTGCGCTCACTGCGCCGCTTTCCAGTCGCGGAACCTGTCTGCCAGCTGCA	240
Db	192	attaatttgcgctgctgcgtcaactgccgctttctcagtcgggaacacctgcgtgccagctgca	251
QY	241	TTAATGAATCGGCCAACCGCGGGGAGAGGGGTTTTCGCTATTTCGGCGCCAGGCTGGTTT	300
Db	252	ttaatgaatcgccaaacgcgcgggagagcggcttgcgtatttgggcgccagggtggttt	311
QY	301	TTCTTTTACCACTGAGACGGGCAACAGCTGATTGCCCTTACCGCTGGCCCTTGAGAGA	360
Db	312	ttcttttcaccagctgagagacgggcaacagctgattgccttcaccgcgctggccctgagaga	371
QY	361	GTTGCAGCAAGCGGTCCACGCTGGTTTGGCCCCAGCAGCGCAAAATCCTGTTGATGGTGG	420
Db	372	gttgacagcaagcgtgccacgcgtggtttgccccagagggcaaatccctgtttgatggctg	431
QY	421	TTCCGAAATTCGCAAAATCCCTTATAAATCAAAGAATAGCCCGAGATAGGGTTGAGTGT	480
Db	432	ttccgaaaatcggcadaaatccctctataaatcaaaagaaatagcccgagataggggttgagtgt	491
QY	481	TGTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTTGGACTCCCAACGTCACAAAGGCG	540
Db	492	tgttccagtttggaaacaagantccactattaagaagaacgtgggactcccaacgctcaaaagggcg	551
QY	541	AAAAACCGCTATACGAGCGGATGGCCCCACTACGTGAACCATCACCCAA	588
Db	552	aaaaa-cgtctatcaggcgatcgccccactacgtgaaccatcacccaa	591

US-09-334-818A-11
Sequence 11, Application US/09334818A

RESULT 12

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US-09-334-818A-22
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: Sequence 22, Application US/09334818A
: GENERAL INFORMATION:
:
: APPLICANT: DAVIS, MARIA
: APPLICANT: FULLER, CARL W.
: APPLICANT: MAMONE, JOSEPH A.
: APPLICANT: HUANG, LIN
:
: TITLE OF INVENTION: FY7 POLYMERASE
:
: FILE REFERENCE: PB9817
:
: CURRENT APPLICATION NUMBER: US/09/334,818A
:
: PRIOR FILING DATE: 1998-06-17
:
: PRIOR APPLICATION NUMBER: 60/089,556
:
: PRIOR FILING DATE: 1998-06-17
:
: NUMBER OF SEQ ID NOS: 27
:
: SOFTWARE: Patent In Ver. 2.1

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SEQ ID NO 22
LENGTH: 602
TYPE: DNA
ORGANISM: Thermus sp.
FEATURE:
NAME/KEY: modified_base
LOCATION: (2)
OTHER INFORMATION: a, t, c or g
FEATURE:
NAME/KEY: modified_base
LOCATION: (569)
OTHER INFORMATION: a, t, c or g
FEATURE:
NAME/KEY: modified_base
LOCATION: (585)
OTHER INFORMATION: a, t, c or g
S-09-334-81.8A-22

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Query Match 47.0%; Score 572.4; DB 5;
Best Local Similarity 99.3%;
Matches 584; pred. NO. 8.2e-154;
Length 602;

1 GCCAAGCTTGCATGCGCTGCAGGTCGACTCTAGAGGATCCCCGGGTACCGAGCTCGAATTC 60

I; Gaps

r; runders

I; gaps

61 GTAAATCATGTCATAGCTGTTTCCCTCTGTGCAATGTTTATCCGCTCACAAATTCACACAA 120
|||||
72 gaatcatggtcatagctgtttccctgtgcaatgttattccgcgtccacaattccacaaa 131

72 gtaatcagggtcatagctgtttcctgtgaaattgttatccggtcaccaattccacaa 131

Thu Aug 1 12:08:41 2002

NAME/KEY: modified_base
LOCATION: (16)
OTHER INFORMATION: a, t, c or g
FEATURE:
NAME/KEY: modified_base
LOCATION: (405)
OTHER INFORMATION: a, t, c or g
FEATURE:
NAME/KEY: modified_base
LOCATION: (512)
OTHER INFORMATION: a, t, c or g
US-09-334-818A-18

Query Match 46.3%; Score 564; DB 5; Length 601;
Best Local Similarity 99.0%; Pred. No. 2.1e-151;
Matches 586; Conservative 0; Mismatches 4; Indels 2; Gaps 2;

QY 1 GCCAAGCTTCATGCC-TGCAGGTCGACTCTAGAGATCCCCGGGTACCGAGCTCGAATT 59
Db 11 gccnancctgcatgcttgcaggtcgcactctagagatccccgggtaccgagctcgaatt 70
QY 60 CGTAATCATGGTCATAGCTGTTTCCCTGTGTGAAATTTATCCGCTCACAAATTCACACA 119
Db 71 cgtaatcatggtcatagctgtttctctgtgaaattgtatccgctcacattccacaca 130
QY 120 ACATACGAGCGGGAAGCATAAAGTGTAAAGCTGGGTGCTTAATGAGTGAAGTAACTCA 179
Db 131 acatacagcgccggaagcataaagtgtaaagcctgggtgcttaataatgagtgagctca 190
QY 180 CATTAATTCGCTGGCTCACTGCGCGCTTTCCAGTTCGGGAAACCTGTCGTCGAGCTGC 239
Db 191 cattaatgctgtgctgctcaactgcccgtttccagtcgggaaacctgtcgtgcccagctgc 250
QY 240 ATTAATGAATCGGCCAACCGCGGGAGAGCGCGTTCGCTATTGGCGCCGAGGGTGGTT 299
Db 251 attaatgaatcgcccaagcgcgggagagcggtttgctatttggcgccaggggtgtt 310
QY 300 TTTCTTTTCCAGCTGAGACGGCAACAGCTGATTGCCCTTCCCGCTGGCCCTGAGAG 359
Db 311 ttctctttccacagtgagacggcggaacagctgattgctctccagctggccctgagag 370
QY 360 AGTTGCAGCAAGCGTCCACGCTGTTGCCCGCAGCGGAAATCCTGTTTGTGAGTGTG 419
Db 371 agttgcagcaagcggtccacgctggtttgcccccacagcggaataatcctgttggatgg 430
QY 420 GTTCCGGAATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGTTGAGTG 479
Db 431 gtcccgaaatcgccaaatcccttataatcaaaagaatagcccgagatagggttggatg 490
QY 480 TTGTTCCAGTTTGGACAAGAGTCCACTATTAAAGACGTGGACTCCCAAGCTCAAGGGC 539
Db 491 ttgttccagtttggaaagaagantccactattaaagaacgtggagactcaacgtcaaaagg 550
QY 540 GAAAAACGCTATCAGGGCGCTGCGCCACTGACCTAGTGAACCATCACCAATC 591
Db 551 gaaaaaccgtctctacagggcgat-gccactacgtgaaccatcaccccaatc 601

RESULT 14
US-09-334-818A-5
; Sequence 5, Application US/09334818A
; GENERAL INFORMATION:
; APPLICANT: DAVIS, MARIA
; APPLICANT: FULLER, CARL W.
; APPLICANT: MAMONE, JOSEPH A.
; APPLICANT: HUANG, LIN
; TITLE OF INVENTION: FY7 POLYMERASE
; FILE REFERENCE: PB9817
; CURRENT APPLICATION NUMBER: US/09/334,818A
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/089,556
; PRIOR FILING DATE: 1998-06-17

Db 9 gccaaagcttgcagctgcaggtcagactctagagatccccgggtaccgagctcgaattc 68
QY 61 GTAATCATGGTCATAGCTGTTTCCCTGTGTGAAATTTATCCGCTCACAAATTCACACAA 120
Db 69 gtaaatcatggtcatagctgtttctctgtgaaattgttatccgctcacattccacacaa 128
QY 121 CATACAGCGGAGCATAAAGTAAAGCTGGGTGCTTAATGAGTGAAGTAACTAC 180
Db 129 catacagcggaagcataaagtataagcctgggtgcttaagtgtgagctaaactcac 188
QY 181 ATTAATTCGCTTCGCTCACTGCCGCTTTCCAGTGGGGAACCTGCTGTCGACGCTGCA 240
Db 189 attaatgctgtgctcactgcccgtttccagtcgggaaacctgtcgtgccagctgca 248
QY 241 TTAATGAATCGGCCAACCGCGGAGAGCGGTTTTCGCTATTGGGCGCCAGGGTGGTTT 300
Db 249 ttaatgaatcgcccaacgccccgagagagcggttgcgtattggtggcgccaggggtggtt 308
QY 301 TTTCTTTTCCAGCTGAGACGGGCAACAGCTGATTGGCCCTTCACCGCTGGCCCTGAGAGA 360
Db 309 ttctttccacagtgagacgggcaacagctgattgcccctccacgctgccccctgagaga 368
QY 361 GTTCAGCAAGCGGTCACGCTGTTTGGCCCGCAGCAGCGGAAATPCCTGTTGATGTGG 420
Db 369 gttgcagcaagcggtccacgctgtgttggcccagcagcggaataatcctgtttgattgt 428
QY 421 TTTCCGAAATCGCAAAATCCCTTATAATCAAAAGAAATAGCCGAGATAGGCTTGAAGT 480
Db 429 ttccgaaatcgccaaatcccttataatcaaaagaatagccccgagatagggttgatgt 488
QY 481 TGTTCAGTTTGGACAAGAGTCCACTATTAAAGACGTGGACTCCACGCTCAAGGGCGG 540
Db 489 tgttcagtttggaaacaga-tccactattaaagaacgtggactccacagtcacaaaggcg 547
QY 541 AAAAAACGCTATCAGGGCGATGGCCACTACGTGACCATCACCCCA 588
Db 548 aaaaaccgtctatcagggcgangggccactacgtgaancatcaccaaa 595

RESULT 13
US-09-334-818A-18
; Sequence 18, Application US/09334818A
; GENERAL INFORMATION:
; APPLICANT: DAVIS, MARIA
; APPLICANT: FULLER, CARL W.
; APPLICANT: MAMONE, JOSEPH A.
; APPLICANT: HUANG, LIN
; TITLE OF INVENTION: FY7 POLYMERASE
; FILE REFERENCE: PB9817
; CURRENT APPLICATION NUMBER: US/09/334,818A
; PRIOR FILING DATE: 1999-06-17
; PRIOR APPLICATION NUMBER: 60/089,556
; PRIOR FILING DATE: 1998-06-17
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Thermus sp.
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (1)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)
; OTHER INFORMATION: a, t, c or g
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (14)
; OTHER INFORMATION: a, t, c or g
; FEATURE:

us-10-014-743-1.rnpn

Thu Aug 1 12:08:41 2002

Thu Aug 1 12:08:45 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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Title: us-10-014-743-2

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- 73: /cgn2_6/ptodata/1/pna/US6034_COMB.seq.*
- 74: /cgn2_6/ptodata/1/pna/US6035_COMB.seq.*
- 75: /cgn2_6/ptodata/1/pna/US6036_COMB.seq.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	18	100.0	18	1	PCT-US00-07945-5	Sequence 5, Appl
2	18	100.0	18	1	PCT-US00-33547-465	Sequence 465, Appl
3	18	100.0	18	1	PCT-US00-34970-12	Sequence 12, Appl
4	18	100.0	18	1	PCT-US01-04064-39	Sequence 39, Appl
5	18	100.0	18	1	PCT-US01-06056-9	Sequence 9, Appl
6	18	100.0	18	1	PCT-US01-06516-10	Sequence 10, Appl
7	18	100.0	18	1	PCT-US01-08961-84	Sequence 84, Appl
8	18	100.0	18	1	PCT-US01-09718-134	Sequence 134, Appl
9	18	100.0	18	1	PCT-US01-10298-49	Sequence 49, Appl
10	18	100.0	18	1	PCT-US01-10666-124	Sequence 124, Appl
11	18	100.0	18	1	PCT-US01-10671-49	Sequence 54, Appl
12	18	100.0	18	1	PCT-US01-10742-174	Sequence 174, Appl
13	18	100.0	18	1	PCT-US01-11509-130	Sequence 130, Appl
14	18	100.0	18	1	PCT-US01-11853-79	Sequence 79, Appl
15	18	100.0	18	1	PCT-US01-11943-34	Sequence 34, Appl
16	18	100.0	18	1	PCT-US01-12011-49	Sequence 49, Appl
17	18	100.0	18	1	PCT-US01-12254A-49	Sequence 49, Appl
18	18	100.0	18	1	PCT-US01-12257-79	Sequence 79, Appl
19	18	100.0	18	1	PCT-US01-12268-29	Sequence 29, Appl
20	18	100.0	18	1	PCT-US01-12302-39	Sequence 39, Appl
21	18	100.0	18	1	PCT-US01-12303-74	Sequence 74, Appl
22	18	100.0	18	1	PCT-US01-12305-49	Sequence 49, Appl
23	18	100.0	18	1	PCT-US01-12453-69	Sequence 69, Appl
24	18	100.0	18	1	PCT-US01-14715-64	Sequence 64, Appl
25	18	100.0	18	1	PCT-US01-14717-39	Sequence 39, Appl
26	18	100.0	18	1	PCT-US01-14772-19	Sequence 19, Appl
27	18	100.0	18	1	PCT-US01-14773-19	Sequence 25, Appl
28	18	100.0	18	1	PCT-US01-15789-25	Sequence 25, Appl
29	18	100.0	18	1	PCT-US01-16045-71	Sequence 71, Appl
30	18	100.0	18	1	PCT-US01-16278-24	Sequence 24, Appl
31	18	100.0	18	1	PCT-US01-16280-99	Sequence 99, Appl

32 18 100.0 18 1 PCT-US01-16350A-34 Sequence 34, Appl
33 18 100.0 18 1 PCT-US01-16352-89 Sequence 89, Appl
34 18 100.0 18 1 PCT-US01-16905-34 Sequence 34, Appl
35 18 100.0 18 1 PCT-US01-17252-124 Sequence 124, Appl
36 18 100.0 18 1 PCT-US01-17994-79 Sequence 79, Appl
37 18 100.0 18 1 PCT-US01-18811A-54 Sequence 54, Appl
38 18 100.0 18 1 PCT-US01-18813-54 Sequence 54, Appl
39 18 100.0 18 1 PCT-US01-18814-60 Sequence 60, Appl
40 18 100.0 18 1 PCT-US01-19447A-37 Sequence 37, Appl
41 18 100.0 18 1 PCT-US01-19835-89 Sequence 89, Appl
42 18 100.0 18 1 PCT-US01-20951-59 Sequence 59, Appl
43 18 100.0 18 1 PCT-US01-20952-79 Sequence 79, Appl
44 18 100.0 18 1 PCT-US01-21064-64 Sequence 64, Appl
45 18 100.0 18 1 PCT-US01-21306-139 Sequence 139, Appl

ALIGNMENTS

RESULT 1
PCT-US00-07945-5
; Sequence 5, Application PC/TUS0007945
; GENERAL INFORMATION:
; APPLICANT: Patricia Billing-Medel
; APPLICANT: Maurice Cohen
; APPLICANT: Tracey L. Colpitts
; APPLICANT: Julian Gordon
; APPLICANT: Edward N. Granados
; APPLICANT: John C. Russell
; APPLICANT: Stephen D. Stroupe
; TITLE OF INVENTION: Reagents and Methods Useful for
; TITLE OF INVENTION: Detecting Disease of the Prostate
; FILE REFERENCE: 6397.PC.01
; CURRENT APPLICATION NUMBER: PCT/US00/07945
; CURRENT FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 09/276,600
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Universal primer
PCT-US00-07945-5

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAAACGACGCGCCAGT 18
Db 1 TGTAAACGACGCGCCAGT 18
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RESULT 2
PCT-US00-33547-465
; Sequence 465, Application PC/TUS0033547
; GENERAL INFORMATION:
; APPLICANT: COGENT NEUROSCIENCE, Inc.
; APPLICANT: Lo, Donald C.
; APPLICANT: Barney, Shawn
; APPLICANT: Thomas, Mary Beth
; APPLICANT: Porthury, Stuart D.
; APPLICANT: Purnanani, Kasturi
; APPLICANT: Katz, Lawrence C.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSING
; TITLE OF INVENTION: AND TREATING CONDITIONS, DISORDERS, OR DISEASES INVOLVING
; TITLE OF INVENTION: CELL DEATH
; FILE REFERENCE: 10001-005-228
; CURRENT APPLICATION NUMBER: PCT/US00/33547

; CURRENT FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 09/461,697
; PRIOR FILING DATE: 1999-12-14
; NUMBER OF SEQ ID NOS: 466
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
PCT-US00-33547-465

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAAACGACGCGCCAGT 18
Db 1 TGTAAACGACGCGCCAGT 18
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RESULT 3
PCT-US00-34970-12
; Sequence 12, Application PC/TUS0034970
; GENERAL INFORMATION:
; APPLICANT: BASF PLANT SCIENCE GMBH
; TITLE OF INVENTION: PROTEIN KINASE STRESS-RELATED PROTEINS AND METHODS OF
; FILE REFERENCE: 16313-0007
; CURRENT APPLICATION NUMBER: PCT/US00/34970
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/171,745
; PRIOR FILING DATE: 1999-12-22
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
PCT-US00-34970-12

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAAACGACGCGCCAGT 18
Db 1 TGTAAACGACGCGCCAGT 18
|||||

RESULT 4
PCT-US01-04064-39
; Sequence 39, Application PC/TUS0104064
; GENERAL INFORMATION:
; APPLICANT: Peter J. Oefner
; TITLE OF INVENTION: DETECTION OF POLYMORPHISMS BY DENATURING
; FILE REFERENCE: STAN-174WO
; CURRENT APPLICATION NUMBER: PCT/US01/04064
; CURRENT FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 39
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic oligonucleotide

us-10-014-743-2.rnmpm

Thu Aug 1 12:08:45 2002

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PCT-US01-04064-39

Query Match          100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCGCCAGT 18
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Db 1 tgtaaaacgacgcccagt 18

RESULT 5
PCT-US01-06056-9
; Sequence 9, Application PC/TUS0106056
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Chew, Anne
; APPLICANT: Denton, R. Rex
; APPLICANT: Nandabalan, Krishnan
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: HAPLOTYPES OF THE DRD1 GENE
; FILE REFERENCE: MH-0057PCT DR1
; CURRENT APPLICATION NUMBER: PCT/US01/06056
; CURRENT FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 60/184,922
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; TYPE: DNA
; ORGANISM: Homo sapiens
; PCT-US01-06056-9

Query Match          100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCGCCAGT 18
    |||
Db 1 tgtaaaacgacgcccagt 18

PCT-US01-06516-10
; Sequence 10, Application PC/TUS0106516
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Billing-Medel, Patricia A.
; APPLICANT: Cohen, Maurice
; APPLICANT: Colpitts, Tracey L.
; APPLICANT: Friedman, Paula N.
; APPLICANT: Gordon, Julian
; APPLICANT: Granados, Edward N.
; APPLICANT: Hodges, Steven C.
; APPLICANT: Klass, Michael R.
; APPLICANT: Kratochvil, Jon D.
; APPLICANT: Roberts-Rapp, Lisa
; APPLICANT: Russell, John C.
; APPLICANT: Scroupe, Stephen D.
; TITLE OF INVENTION: Reagents And Method Useful For Detecting
; FILE REFERENCE: 5995.US.P2
; CURRENT APPLICATION NUMBER: PCT/US01/06516
; CURRENT FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 08/962,094
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: US 08/742,667
; PRIOR FILING DATE: 1996-10-31

PCT-US01-06516-10
; Sequence 134, Application PC/TUS0109718
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Koshiy, Beena
; APPLICANT: Kliehm, Stefanie E.
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Choi, Julie Y.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Anastasio, Allison E.
; TITLE OF INVENTION: HAPLOTYPES OF THE FKBP8 GENE
; FILE REFERENCE: MH-0072 PCT FKBP8
; CURRENT APPLICATION NUMBER: PCT/US01/09718
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/192,125
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134

PCT-US01-08961-84
; Sequence 84, Application PC/TUS0108961
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Stephen C.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Koshiy, Beena
; APPLICANT: Kliehm, Stephanie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE GNB3 GENE
; FILE REFERENCE: MH-0069PCT GNB3
; CURRENT APPLICATION NUMBER: PCT/US01/08961
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/190,986
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; TYPE: DNA
; ORGANISM: Homo sapien
; PCT-US01-08961-84

Query Match          100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCGCCAGT 18
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Db 1 tgtaaaacgacgcccagt 18

PCT-US01-08961-84
; Sequence 84, Application PC/TUS0108961
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Stephen C.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Koshiy, Beena
; APPLICANT: Kliehm, Stephanie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE GNB3 GENE
; FILE REFERENCE: MH-0069PCT GNB3
; CURRENT APPLICATION NUMBER: PCT/US01/08961
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/190,986
; PRIOR FILING DATE: 2000-03-21
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 84
; TYPE: DNA
; ORGANISM: Homo sapien
; PCT-US01-08961-84

Query Match          100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCGCCAGT 18
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Db 1 tgtaaaacgacgcccagt 18

PCT-US01-09718-134
; Sequence 134, Application PC/TUS0109718
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Koshiy, Beena
; APPLICANT: Kliehm, Stefanie E.
; APPLICANT: Stephens, J. Claiborne
; APPLICANT: Choi, Julie Y.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Anastasio, Allison E.
; TITLE OF INVENTION: HAPLOTYPES OF THE FKBP8 GENE
; FILE REFERENCE: MH-0072 PCT FKBP8
; CURRENT APPLICATION NUMBER: PCT/US01/09718
; CURRENT FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/192,125
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 136
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 134
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; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-09718-134

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
|||||
Db 1 tgtaaaacgacggccagt 18

RESULT 9
PCT-US01-10298-49
; Sequence 49, Application PC/TUS0110298
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Denton, R. Rex
; TITLE OF INVENTION: HAPLOTYPES OF THE GSTM3 GENE
; FILE REFERENCE: MMH-0414PCT GSTM3
; CURRENT APPLICATION NUMBER: PCT/US01/10298
; PRIOR FILING DATE: 2001-03-30
; PRIOR FILING DATE: 2000-04-13
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-10298-49

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
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Db 1 tgtaaaacgacggccagt 18

RESULT 10
PCT-US01-10666-124
; Sequence 124, Application PC/TUS0110666
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Klem, Stefanie C.
; APPLICANT: Koshi, Beena
; APPLICANT: Lee, Helen H.
; APPLICANT: Sanchis, Angela
; TITLE OF INVENTION: HAPLOTYPES OF THE CHRN2 GENE
; FILE REFERENCE: MMH-0301PCT CHRN2
; CURRENT APPLICATION NUMBER: PCT/US01/10666
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; PRIOR FILING DATE: 2000-07-13
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 124
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-10666-124

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
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Db 1 tgtaaaacgacggccagt 18

RESULT 11
PCT-US01-10670-54
; Sequence 54, Application PC/TUS0110670
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Klem, Stefanie E.
; APPLICANT: Koshi, Beena
; TITLE OF INVENTION: HAPLOTYPES OF THE APOA4 GENE
; FILE REFERENCE: MMH-0506PCT APOA4
; CURRENT APPLICATION NUMBER: PCT/US01/10670
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2000-04-05
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-10670-54

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
|||||
Db 1 tgtaaaacgacggccagt 18

RESULT 12
PCT-US01-10671-49
; Sequence 49, Application PC/TUS0110671
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Choi, Julie Y.
; APPLICANT: Klem, Stefanie E.
; APPLICANT: Koshi, Beena
; APPLICANT: Parks, Katie E.
; TITLE OF INVENTION: HAPLOTYPES OF THE GPIA GENE
; FILE REFERENCE: MMH-0260PCT GPIA
; CURRENT APPLICATION NUMBER: PCT/US01/10671
; PRIOR FILING DATE: 2001-04-03
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 49
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-10671-49

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18

us-10-014-743-2.rnppm

Thu Aug 1 12:08:45 2002

Db 1 tgtaaacgacgagccagt 18
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RESULT 13
PCT-US01-10742-174
; Sequence 174, Application PC/TUS0110742
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Koshi, Beena
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Anastasio, Alison E.
; APPLICANT: Chew, Anne
; APPLICANT: Rounds, Eileen
; APPLICANT: Parks, Katie
; APPLICANT: Choi, Julie Y.
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: HAPLOTYPES OF THE GLC1C GENE
; FILE REFERENCE: MWH-0145 PCT GLC1C
; CURRENT APPLICATION NUMBER: PCT/US01/10742
; CURRENT FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 60/194,305
; PRIOR FILING DATE: 2000-04-03
; NUMBER OF SEQ ID NOS: 176
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 174
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-10742-174

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAACGACGAGCCAGT 18
|||||
Db 1 tgtaaacgacgagccagt 18

RESULT 14
PCT-US01-11509-130
; Sequence 130, Application PC/TUS0111509
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Chew, Anne
; APPLICANT: Koshi, Beena
; APPLICANT: Stephens, J. Claiborne
; TITLE OF INVENTION: HAPLOTYPES OF THE CALM1 GENE
; FILE REFERENCE: MWH-0102PCT CALM1
; CURRENT APPLICATION NUMBER: PCT/US01/11509
; CURRENT FILING DATE: 2001-04-09
; PRIOR APPLICATION NUMBER: 60/196,340
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 133
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 130
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapien
PCT-US01-11509-130

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAACGACGAGCCAGT 18
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Db 1 tgtaaacgacgagccagt 18

RESULT 15
PCT-US01-11853-79
; Sequence 79, Application PC/TUS0111853
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Chew, Anne
; APPLICANT: Choi, Julie Y.
; APPLICANT: Kazemi, Amir
; APPLICANT: Koshi, Beena
; TITLE OF INVENTION: Haplotypes of the ACHE Gene
; FILE REFERENCE: MWH-0509PCT ACHE
; CURRENT APPLICATION NUMBER: PCT/US01/11853
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 60/197,173
; PRIOR FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 79
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-11853-79

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAACGACGAGCCAGT 18
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Db 1 tgtaaacgacgagccagt 18

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Job time: 11351 sec

Thu Aug 1 12:08:45 2002

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 11:04:49 ; Search time 348.01 Seconds
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Title: us-10-014-743-2

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Post-processing: Minimum Match 0%

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- 3: /cgn2_6/ptodata/1/pna/US07_NEW_COMB.seq.*
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- 5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq.*
- 6: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq.*
- 7: /cgn2_6/ptodata/1/pna/US10_NEW_COMB.seq2.*
- 8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	18	100.0	18	1	PCT-US02-12314-49
2	18	100.0	18	1	PCT-US02-13013-54
3	18	100.0	18	1	PCT-US02-13014-44
4	18	100.0	18	1	PCT-US02-12994-69
5	18	100.0	18	1	PCT-US02-14004-89
6	18	100.0	18	1	PCT-US02-14010-24
7	18	100.0	18	1	PCT-US02-14011-109
8	18	100.0	18	1	PCT-US02-14038-19
9	18	100.0	18	1	PCT-US02-14540-54
10	18	100.0	18	1	PCT-US02-15638-54
11	18	100.0	18	1	PCT-US02-15657-64
12	18	100.0	18	1	PCT-US01-46100A-69
13	18	100.0	18	1	PCT-US01-47011A-64
14	18	100.0	18	5	US-09-636-259A-15
15	18	100.0	18	5	US-09-120-051C-10
16	18	100.0	18	5	US-09-345-882-139
17	18	100.0	18	5	US-09-889-914A-3
18	18	100.0	18	5	US-09-431-384B-10
19	18	100.0	18	5	US-09-120-051D-10
20	18	100.0	18	6	US-10-185-567-14
21	18	100.0	18	6	US-10-192-254-13
22	18	100.0	18	6	US-10-191-045-124
23	18	100.0	18	6	US-10-069-439A-3
24	18	100.0	18	6	US-10-188-498-174
25	18	100.0	18	6	US-10-188-498-174

Sequence 34, Appl
Sequence 16, Appl
Sequence 4, Appl
Sequence 25, Appl
Sequence 139, Appl
Sequence 71, Appl
Sequence 6, Appl
Sequence 3, Appl
Sequence 49, Appl
Sequence 29, Appl
Sequence 28, Appl
Sequence 49, Appl
Sequence 64, Appl
Sequence 124, Appl
Sequence 104, Appl
Sequence 109, Appl
Sequence 1, Appl
Sequence 44, Appl
Sequence 589, Appl

ALIGNMENTS

RESULT 1
PCT-US02-12314-49
; Sequence 49, Application PC/TUS0212314
; GENERAL INFORMATION:
; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Denton, R. Rex
; APPLICANT: Gilson, Christopher
; APPLICANT: Lee, Helen
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE CHRM1 GENE
; FILE REFERENCE: CHRM1_MWH-0015PCT2
; CURRENT APPLICATION NUMBER: PCT/US02/12314
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: 60/159,269
; PRIOR FILING DATE: 1999-10-13
; PRIOR APPLICATION NUMBER: PCT/US00/28211
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 49
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-12314-49

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TGTAAACGACGCCAGT 18
Db 1 tgtaaacgacgccagct 18
|||||

RESULT 2
PCT-US02-13013-54
; Sequence 54, Application PC/TUS0213013
; GENERAL INFORMATION:
; APPLICANT: Genassance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Parks, Katie
; APPLICANT: Sausker, Elizabeth
; TITLE OF INVENTION: HAPLOTYPES OF THE NRL GENE
; FILE REFERENCE: NRL_MWH-0180PCT
; CURRENT APPLICATION NUMBER: PCT/US02/13013

; CURRENT FILING DATE: 2001-04-22
; PRIOR APPLICATION NUMBER: 60/285,142
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-13013-54

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
|||||
Db 1 tgtaaacgacgcccagt 18

RESULT 3
PCT-US02-13014-44
; Sequence 44, Application PC/TUS0213014
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE THPO GENE
; FILE REFERENCE: THPO_MWH-0528PCT
; CURRENT APPLICATION NUMBER: PCT/US02/13014
; CURRENT FILING DATE: 2002-04-22
; PRIOR APPLICATION NUMBER: 60/285,279
; PRIOR FILING DATE: 2001-04-20
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-13014-44

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
|||||
Db 1 tgtaaacgacgcccagt 18

RESULT 4
PCT-US02-12994-69
; Sequence 69, Application PC/TUS0212994
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Lee, Helen
; APPLICANT: Sausker, Elizabeth
; TITLE OF INVENTION: HAPLOTYPES OF THE HCF2 GENE
; FILE REFERENCE: HCF2_MWH-0152PCT
; CURRENT APPLICATION NUMBER: PCT/US02/12994
; CURRENT FILING DATE: 2002-04-23
; PRIOR APPLICATION NUMBER: 60/285,871
; PRIOR FILING DATE: 2001-04-23
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69

; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-12994-69

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
|||||
Db 1 tgtaaacgacgcccagt 18

RESULT 5
PCT-US02-14004-89
; Sequence 89, Application PC/TUS0214004
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Rounds, Eileen
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE RXRB GENE
; FILE REFERENCE: MWH-0480PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14004
; CURRENT FILING DATE: 2002-05-01
; PRIOR APPLICATION NUMBER: 60/287,960
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 89
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14004-89

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
|||||
Db 1 tgtaaacgacgcccagt 18

RESULT 6
PCT-US02-14010-24
; Sequence 24, Application PC/TUS0214010
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Gilson, Christopher
; APPLICANT: Kliem, Stephanie E.
; APPLICANT: Koshi, Beena
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE CRH GENE
; FILE REFERENCE: MWH-0249PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14010
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/288,476
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14010-24

Query Match 100.0%; Score 18; DB 1; Length 18;

us-10-014-743-2.rnpn

Thu Aug 1 12:08:45 2002

Best Local Similarity 100.0%; Pred. No. 0.33; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
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Db 1 tgtaaacgacgagccagt 18

RESULT 7
PCT-US02-14011-109
; Sequence 109, Application PC/TUS0214011
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bentivegna, Steven C.
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Sanchis, Angela
; APPLICANT: Sausker, Elizabeth Ann
; TITLE OF INVENTION: HAPLOTYPES OF THE RXRA GENE
; FILE REFERENCE: MWH-0858PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14011
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: 60/288,475
; PRIOR FILING DATE: 2001-05-03
; NUMBER OF SEQ ID NOS: 111
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14011-109

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgtaaacgacgagccagt 18

RESULT 8
PCT-US02-14538-19
; Sequence 19, Application PC/TUS0214538
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher
; APPLICANT: Kazemi, Amir
; APPLICANT: Koshi, Beena
; TITLE OF INVENTION: HAPLOTYPES OF THE NNMT GENE
; FILE REFERENCE: MWH-0179PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14538
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 30/289,335
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14538-19

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgtaaacgacgagccagt 18

RESULT 9
PCT-US02-14540-54
; Sequence 54, Application PC/TUS0214540
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Allison
; APPLICANT: Chew, Anne
; APPLICANT: Gilson, Christopher
; APPLICANT: Koshi, Beena
; APPLICANT: Sausker, Elizabeth
; TITLE OF INVENTION: HAPLOTYPES OF THE CYP2E GENE
; FILE REFERENCE: CYP2E.MWH-0287PCT
; CURRENT APPLICATION NUMBER: PCT/US02/14540
; CURRENT FILING DATE: 2002-05-07
; PRIOR APPLICATION NUMBER: 60/289,330
; PRIOR FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-14540-54

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgtaaacgacgagccagt 18

RESULT 10
PCT-US02-15638-54
; Sequence 54, Application PC/TUS0215638
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bieglecki, Karyn M.
; APPLICANT: Denton, R. Rex
; APPLICANT: Lee, Helen H.
; APPLICANT: Nandabalan, Krishnan
; TITLE OF INVENTION: HAPLOTYPES OF THE IL8RA GENE
; FILE REFERENCE: MWH-0441PCT
; CURRENT APPLICATION NUMBER: PCT/US02/15638
; CURRENT FILING DATE: 2002-05-15
; PRIOR APPLICATION NUMBER: 60/291,533
; PRIOR FILING DATE: 2001-05-16
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 54
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-15638-54

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGCCAGT 18
| | | | | | | | | | | | | | | | | | | | | |
Db 1 tgtaaacgacgagccagt 18

RESULT 11
PCT-US02-15657-64
; Sequence 64, Application PC/TUS0215657
; GENERAL INFORMATION:

; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Anastasio, Alison
; APPLICANT: Rounds, Eileen
; APPLICANT: Sanchis, Angela
; APPLICANT: Shah, Nisha
; TITLE OF INVENTION: HAPLOTYPES OF THE GPX2 GENE
; FILE REFERENCE: GPX2_MWH-2132PCT
; CURRENT APPLICATION NUMBER: PCT/US02/15657
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/292,394
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US02-15657-64

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 tgtaaacgacggccagt 18

RESULT 12
PCT-US01-46100A-69
; Sequence 69, Application PC/TUS0146100A
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Kazemi, Amir
; APPLICANT: Shah, Nisha
; TITLE OF INVENTION: HAPLOTYPES OF THE CER1 GENE
; FILE REFERENCE: CER1_MWH-1635PCT
; CURRENT APPLICATION NUMBER: PCT/US01/46100A
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/241,634
; PRIOR FILING DATE: 2000-10-19
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-46100A-69

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 tgtaaacgacggccagt 18

RESULT 13
PCT-US01-47011A-64
; Sequence 64, Application PC/TUS0147011A
; GENERAL INFORMATION:
; APPLICANT: Genaisance Pharmaceuticals, Inc.
; APPLICANT: Bleglecki, Karyn M
; APPLICANT: Chew, Anne
; APPLICANT: Russo, David P
; TITLE OF INVENTION: HAPLOTYPES OF THE SAH GENE
; FILE REFERENCE: SAH_MWH-1881PCT
; CURRENT APPLICATION NUMBER: PCT/US01/47011A
; CURRENT FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/250,441

; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US01-47011A-64

Query Match 100.0%; Score 18; DB 1; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 tgtaaacgacggccagt 18

RESULT 14
US-09-636-259A-15
; Sequence 15, Application US/09636259A
; GENERAL INFORMATION:
; APPLICANT: Small, Kersten M
; APPLICANT: Liggett, Stephen
; TITLE OF INVENTION: Alpha-2A-adrenergic receptor polymorphisms
; FILE REFERENCE: 13092
; CURRENT APPLICATION NUMBER: US/09/636,259A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-636-259A-15

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TGTAAACGACGGCCAGT 18
|||||
Db 1 tgtaaacgacggccagt 18

RESULT 15
US-09-120-051C-10
; Sequence 10, Application US/09120051C
; GENERAL INFORMATION:
; APPLICANT: Glisson, John Robert
; APPLICANT: Luo, Yungang
; TITLE OF INVENTION: DNA encoding the outer membrane protein of Pasteurella multocida
; FILE REFERENCE: 757,003US1
; CURRENT APPLICATION NUMBER: US/09/120,051C
; CURRENT FILING DATE: 1998-07-21
; PRIOR FILING DATE: 1997-12-08
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: A primer derived from pUC18
US-09-120-051C-10

Query Match 100.0%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.33;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

us-10-014-743-2.rnpn

Thu Aug 1 12:08:45 2002

QY 1 TCTAAACGACGCCAGT 18
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Db 1 tgtaaacgacggccagt 18

Search completed: August 1, 2002, 11:04:52
Job time: 8687 sec

Thu Aug 1 12:08:49 2002

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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 10:59:20 ; Search time 4897.61 Seconds
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Perfect score: 738
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 21979536 seqs, 10817449327 residues 43959072

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	738	100.0	738	11	US-08-726-462A-3
2	738	100.0	738	37	US-10-014-743-3
3	723	98.0	3253	11	US-08-702-902-6
4	691.8	93.7	3216	17	US-09-347-311-1
5	691.8	93.7	3216	17	US-09-347-311A-1
6	691.8	93.7	3216	37	US-10-057-108-1
7	669.8	90.8	4885	20	US-09-539-698-2
8	669	90.7	4118	14	US-09-068-821-17
9	667.8	90.5	4539	1	PCT-US94-10146-1
10	667.8	90.5	4539	8	US-08-488-015-1
11	667.8	90.5	4539	15	US-09-114-835-1
12	667.8	90.5	4542	17	US-09-399-593A-13
13	667.8	90.5	2571	29	US-09-724-624-93
14	667	90.4	8362	17	US-09-316-175-4
15	666.8	90.4	8362	17	US-09-316-175-8
16	666.8	90.4	10930	4	US-08-090-531-11
17	666.8	90.4	10930	4	US-08-090-531-12
18	666.8	90.4	10930	8	US-08-478-764-11
19	666.8	90.4	10930	8	US-08-478-764-12
20	666.8	90.4	10951	4	US-08-090-531-9
21	666.8	90.4	10951	4	US-08-090-531-10
22	666.8	90.4	10951	8	US-08-478-764-9
23	666.8	90.4	10951	8	US-08-478-764-10
24	666.8	90.4	11296	17	US-09-316-175-1
25	666	90.2	3323	33	US-09-860-763-8
26	666	90.2	3715	33	US-09-860-763-11
27	666	90.2	3774	33	US-09-860-763-9
28	666	90.2	4001	33	US-09-860-763-13
29	666	90.2	4107	33	US-09-860-763-12
30	666	90.2	4162	33	US-09-861-881-1
31	666	90.2	4162	33	US-09-861-881-1

32 666 90.2 4393 33 US-09-861-881-2
33 666 90.2 5148 33 US-09-860-763-10
34 665.8 90.2 6688 26 US-09-667-569A-92
C 36 665.4 90.2 5115 14 US-09-020-716-5
C 37 665.4 90.2 8320 26 US-09-020-716-5
38 665.4 90.2 8320 26 US-09-667-569A-73
C 39 660.4 89.5 10306 1 PCT-US94-03784-4
C 40 660.4 89.5 10306 1 PCT-US94-03784-4
C 41 659.4 89.3 9837 1 PCT-US97-05598-68
C 42 650.8 88.2 4161 1 PCT-US99-25666-6
C 43 650.8 88.2 4161 1 PCT-US99-25666-6
C 44 650.8 88.2 4161 15 US-09-185-143-6
C 45 650.8 88.2 4161 18 US-09-471-913-1

ALIGNMENTS

RESULT 1
US-08-726-462A-3
; Sequence 3, Application US/08726462A
; GENERAL INFORMATION:
; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
; APPLICANT: Division
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED
; TITLE OF INVENTION: FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; ADDRESSEE: & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for windows 6.0,
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08726,462A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: PELM4304
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 738 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-462A-3

Query Match 100.0%; Score 738; DB 11; Length 738;
Best Local Similarity 100.0%; Pred. No. 1.7e-205;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
; 1 ATACGACTACTATAGGCGGAATTCGAGCTCGGTACCGGGGATCTCTAGAGTCGACCT 60

Sequence 2, Appli
Sequence 10, Appl
Sequence 92, Appl
Sequence 5, Appl
Sequence 5, Appl
Sequence 73, Appl
Sequence 72, Appl
Sequence 4, Appl
Sequence 5, Appl
Sequence 68, Appl
Sequence 6, Appl
Sequence 8, Appl
Sequence 6, Appl
Sequence 1, Appl

Db 1 ATACGACTACTATAGGCGGAATTCGAGCTCGGTACCGGGGATCTCTAGAGTCGACCT 60
Qy 61 GCAGGCATGCAAGCTTGAGTATTTCTATAGTGTCACTTAATAAGCTTGGCGTAAATCATGT 120
Db 61 GCAGGCATGCAAGCTTGAGTATTTCTATAGTGTCACTTAATAAGCTTGGCGTAAATCATGT 120
Qy 121 CATAGCTGTTTCCCTGCTGTAATTTGTTATCCGCTCACAAATCCACACACATACGAGCG 180
Db 121 CATAGCTGTTTCCCTGCTGTAATTTGTTATCCGCTCACAAATCCACACACATACGAGCG 180
Qy 181 GAAGCATAAAGTGTAAAGCTTGGGCTGCTTAATGAGTCAGTCACTCAATTAATTTGGT 240
Db 181 GAAGCATAAAGTGTAAAGCTTGGGCTGCTTAATGAGTCAGTCACTCAATTAATTTGGT 240
Qy 241 TGGCTCTACCTGCGCGCTTTCCAGTCGGGAACCTGTGTGCGAGTGCATTAATGAATCG 300
Db 241 TGGCTCTACCTGCGCGCTTTCCAGTCGGGAACCTGTGTGCGAGTGCATTAATGAATCG 300
Qy 301 GCCAACGCGGGGAGAGCGGTTTGGCTATTTGGGCGCTCTTCCGCTTCCGCTCACTG 360
Db 301 GCCAACGCGGGGAGAGCGGTTTGGCTATTTGGGCGCTCTTCCGCTTCCGCTCACTG 360
Qy 361 ACTCGCTGCGCTGCGTTCGCTGCGCTGCGGAGCGGTATCAGTCACTCAAAAGCGGTAA 420
Db 361 ACTCGCTGCGCTGCGTTCGCTGCGCTGCGGAGCGGTATCAGTCACTCAAAAGCGGTAA 420
Qy 421 TAGCGTTATCCAGAAATCAGGGGATTAACGAGCAAGAACATGTGAGCAAAAGCGCAGC 480
Db 421 TAGCGTTATCCAGAAATCAGGGGATTAACGAGCAAGAACATGTGAGCAAAAGCGCAGC 480
Qy 481 AAAAGGCGAGCAACCGTAAAGGCGGCTTGTGCGCTTTTCCATAGGCTCCGCGCCC 540
Db 481 AAAAGGCGAGCAACCGTAAAGGCGGCTTGTGCGCTTTTCCATAGGCTCCGCGCCC 540
Qy 541 CTGAGGAGCATCACAAAATCAGCTCAAGTCAGAGTGGGGAACCGCAGCAGGACTAT 600
Db 541 CTGAGGAGCATCACAAAATCAGCTCAAGTCAGAGTGGGGAACCGCAGCAGGACTAT 600
Qy 601 AAAGATACCGAGGCTTTCCCGCTGGAAGCTCCCTGCGCTCTCTGTTCCGAGCCCTGC 660
Db 601 AAAGATACCGAGGCTTTCCCGCTGGAAGCTCCCTGCGCTCTCTGTTCCGAGCCCTGC 660
Qy 661 CGCTTACCGGATACCTGTCCGCTTTCCTCCCTCGGAGCGGTGGCGGCTTCTCATAGCT 720
Db 661 CGCTTACCGGATACCTGTCCGCTTTCCTCCCTCGGAGCGGTGGCGGCTTCTCATAGCT 720
Qy 721 CACGCTGTAGGTATCTCA 738
Db 721 CACGCTGTAGGTATCTCA 738

RESULT 2
US-10-014-743-3
; Sequence 3, Application US/10014743
; GENERAL INFORMATION:
; APPLICANT: PE Corporation (NY)
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Word 97
; ASCII (DOS) TEXT format

us-10-014-743-3.rnnp

Thu Aug 1 12:08:49 2002

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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/014,743
FILING DATE: 29-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/642,330
FILING DATE: May 3, 1996
APPLICATION NUMBER: 08/672,196
FILING DATE: June 27, 1996
APPLICATION NUMBER: 08/726,462
FILING DATE: October 4, 1996
APPLICATION NUMBER: 09/046,203
FILING DATE: March 23, 1998
APPLICATION NUMBER: 09/272,097
FILING DATE: March 18, 1999
ATTORNEY/AGENT INFORMATION:
NAME: David J. Weltz
REGISTRATION NUMBER: 38,362
REFERENCE/DOCKET NUMBER: 16842-776
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 493-9300
TELEFAX: (650) 493-6811
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 738 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
us-10-014-743-3

Query Match      100.0%; Score 738; DB 37; Length 738;
Best Local Similarity 100.0%; Pred. NO. 1.7e-205;
Matches 738; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATACGACTCCTATAGGCGGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGACCT 60
DB 1 ATACGACTCCTATAGGCGGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGACCT 60
QY 61 GCAGGATGCAAGCTTGTAGTATCTATAGTGCACCTAAATAGCTTGGCGTAATCATGGT 120
DB 61 GCAGGATGCAAGCTTGTAGTATCTATAGTGCACCTAAATAGCTTGGCGTAATCATGGT 120
QY 121 CATAGCTGTTCTGTGTGAATTTGTTATCCGCTCACAATTCACACACATACGAGCG 180
DB 121 CATAGCTGTTCTGTGTGAATTTGTTATCCGCTCACAATTCACACACATACGAGCG 180
QY 181 GAAGCATAAAGTGTAAAGCTGGGTGCCTAATGAGTGAGCTAACTCACTTAATTTGGT 240
DB 181 GAAGCATAAAGTGTAAAGCTGGGTGCCTAATGAGTGAGCTAACTCACTTAATTTGGT 240
QY 241 TGGCTCAGTCCGCGCTTTCCAGTTCGGGAAACCTGCTGCGGAGCTGCAATTAATGATCG 300
DB 241 TGGCTCAGTCCGCGCTTTCCAGTTCGGGAAACCTGCTGCGGAGCTGCAATTAATGATCG 300
QY 301 GCCAACGCGGGGAGAGCGGTTTGGCTATTTGGGCGCTCTTCCGCTTCTCGCTCACTG 360
DB 301 GCCAACGCGGGGAGAGCGGTTTGGCTATTTGGGCGCTCTTCCGCTTCTCGCTCACTG 360
QY 361 ACTGCTCGCTCGGTTCGTTCCGCTGCGGAGCGGATATAGCTCACTCAAGCGGTAA 420
DB 361 ACTGCTCGCTCGGTTCGTTCCGCTGCGGAGCGGATATAGCTCACTCAAGCGGTAA 420
QY 421 TACGGTTATCCACAGAAATCAGGGATACGCGAGGAAGAAACATGTGAGCAAAAGGCCAGC 480
DB 421 TACGGTTATCCACAGAAATCAGGGATACGCGAGGAAGAAACATGTGAGCAAAAGGCCAGC 480
QY 481 AAAGCCGAGGAAACCGTAAAGAGCGGTTGCTGCGGCTTTTTCATAGGCTCCGCCCC 540
DB 481 AAAGCCGAGGAAACCGTAAAGAGCGGTTGCTGCGGCTTTTTCATAGGCTCCGCCCC 540
QY 541 CTGACGAGCATCACAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACGAGGACTAT 600

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DB 541 CTGACGAGCATCACAAAATCGAGCTCAAGTCAGAGTGGCGAAACCCGACGAGGACTAT 600
QY 601 AAGATACCAAGCGGTTTCCCGCTTGGAGCTCCCTCGTGGCGCTCTCTGTTCGACCTGC 660
DB 601 AAGATACCAAGCGGTTTCCCGCTTGGAGCTCCCTCGTGGCGCTCTCTGTTCGACCTGC 660
QY 661 CGCTTACCGGATACCTGTCCGCTTCTCCCTTGGGAAAGCGTGGCGCTTCTCTCATAGCT 720
DB 661 CGCTTACCGGATACCTGTCCGCTTCTCCCTTGGGAAAGCGTGGCGCTTCTCTCATAGCT 720
QY 721 CACGCTGTAGTATCTCA 738
DB 721 CACGCTGTAGTATCTCA 738

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RESULT 3
US-08-702-902-6
; Sequence 6, Application US/08702902
; GENERAL INFORMATION:
; APPLICANT: Belfort, Marlene
; TITLE OF INVENTION: INTEINS AS ANTIMICROBIAL TARGETS:
; TITLE OF INVENTION: GENETIC SCREENS FOR INTEIN FUNCTION
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: Curtis, Morris & Saiford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,902
; FILING DATE: 26-AUG-1996
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454311-2190
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)840-3333
; TELEFAX: (212)840-0712
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3253 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-702-902-6

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Query Match      98.0%; Score 723; DB 11; Length 3253;
Best Local Similarity 100.0%; Pred. NO. 6.9e-201;
Matches 723; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 GGGCGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGAGCTGCGAGCATGCAAGCT 75
DB 55 GGGCGAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGAGCTGCGAGCATGCAAGCT 114
QY 76 TGAGTATCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTCTAGCTGTTCTCTG 135
DB 115 TGAGTATCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTCTAGCTGTTCTCTG 174
QY 136 TGTGAATTTGTATCCGCTCAATTCACACACATACGAGCGGAGGATAAAGTGA 195
DB 175 TGTGAATTTGTATCCGCTCAATTCACACACATACGAGCGGAGGATAAAGTGA 234

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QY 196 AAGCCTGGGTCCTTAATGAGTGAAGTAACTCAATTAATGCGTTCGCTACCTGCGCG 255
Db |||||||
QY 235 AAGCCTGGGTCCTTAATGAGTGAAGTAACTCAATTAATGCGTTCGCTACCTGCGCG 294
Db |||||||
QY 256 CTTTCCAGTCGGGAACCTGCGTCCAGTGCATTAATGAATCGGCAACGCGCGGGA 315
Db |||||||
QY 295 CTTTCCAGTCGGGAACCTGCGTCCAGTGCATTAATGAATCGGCAACGCGCGGGA 354
Db |||||||
QY 316 GAGCGGTTTCGTTATGCGGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGTCGG 375
Db |||||||
QY 355 GAGCGGTTTCGTTATGCGGCTCTTCCGCTTCCTCGCTCACTGACTCGCTGCGTCGG 414
Db |||||||
QY 376 TCGTTCGCTTCGCGGAGCGGTATCACTCACTCAAGGCGTAAATACGTTATCCACAG 435
Db |||||||
QY 415 TCGTTCGCTTCGCGGAGCGGTATCACTCACTCAAGGCGTAAATACGTTATCCACAG 474
Db |||||||
QY 436 AATCAGGGGATACGCGAGGAAGATGTGAGCAAAAGGCGAGCAAGGCGGGAAC 495
Db |||||||
QY 475 AATCAGGGGATACGCGAGGAAGATGTGAGCAAAAGGCGAGCAAGGCGGGAAC 534
Db |||||||
QY 496 GTAAAAGGCGGTTGCTGGGCTTTTCCATAGGCTCGCGCCCTGACGAGCATCACA 555
Db |||||||
QY 535 GTAAAAGGCGGTTGCTGGGCTTTTCCATAGGCTCGCGCCCTGACGAGCATCACA 594
Db |||||||
QY 556 AATCAGGCTCAAGTCAAGGTGGGAAACCGGAGGACTATAAGATACAGGCGT 615
Db |||||||
QY 595 AATCAGGCTCAAGTCAAGGTGGGAAACCGGAGGACTATAAGATACAGGCGT 654
Db |||||||
QY 616 TTCCCGCTGGAAGCTCCCTCGTGGCTCTCTCTGTCGACCTGCGGCTTACCGGATAC 675
Db |||||||
QY 655 TTCCCGCTGGAAGCTCCCTCGTGGCTCTCTCTGTCGACCTGCGGCTTACCGGATAC 714
Db |||||||
QY 676 TGTGCGCTTCTCCCTTGGGAAGCGTGGGCTTTCTCATAGCTCACTGATAGTATC 735
Db |||||||
QY 715 TGTGCGCTTCTCCCTTGGGAAGCGTGGGCTTTCTCATAGCTCACTGATAGTATC 774
Db |||||
QY 736 TCA 738
Db |||||
QY 775 TCA 777

RESULT 4

US-09-347-311-1
; Sequence 1, Application US/09347311
; GENERAL INFORMATION:
; APPLICANT: Plaetnick, Geert
; APPLICANT: Plattewu, Christ
; APPLICANT: Mortier, Katharine
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: Characterisation of Gene Function using dsRNA
; FILE REFERENCE: 50897/002/
; CURRENT APPLICATION NUMBER: US/09/347,311
; EARLIER FILING DATE: 1999-07-02
; EARLIER FILING DATE: 1998-07-03
; EARLIER FILING DATE: 1998-07-03
; EARLIER FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3216
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid DNA
US-09-347-311-1

Query Match 93.7%; Score 691.8; DB 17; Length 3216;
Best Local Similarity 96.2%; Pred. No. 9.8e-192;
Matches 726; Conservative 0; Mismatches 12; Indels 17; Gaps 1;

QY 1 ATACGAGCTACTATPAGGCGGAATTCGAGCTCGGTACCCGGGATCTCTCTAGAGTCGACCT 60
Db |||||||
QY 61 GCAGGC-----ATGCAAGCTTGAATTTCTATATAGTGTACCACTAAATAG 103
Db |||||
QY 104 CTTGGCGTAAATCATGCTCATAGCTGTTCTGTGTAATTTCTATCCCTCACAATTC 163
Db |||||||
QY 164 ACACAACATACGAGCGGAGCATAAAGTGTAAAGCTGGGCTGCTTAATGAGTGAAGT 223
Db |||||||
QY 224 ACTCATTAATTTGGCTTCGCTCACTGCGGCTTTCCAGTCCGGAACCTGTGTCGCA 283
Db |||||||
QY 284 GCTGCTTAAATCAATCGGCCAACGCGGGGAGAGCGGTTTGGCTATTTGGCGCTCTTC 343
Db |||||||
QY 344 CGCTTCTCGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403
Db |||||||
QY 404 TCACCTAAAGCGGCTAATACGCTTATCCACAGATACAGGAGTAACGCGAGGAAGCAAT 463
Db |||||||
QY 464 GTGAGCAAAAGGCGGAGCAAGGAGCAAGGAGCAAGGAGCAAGGAGCAAGGAGCAAT 1165
Db |||||||
QY 524 CCATAGCTCCGCGCTGAGGAGCATACAAAAATCGACGCTCAAGTCAGAGGTGGCG 583
Db |||||||
QY 584 AAACCGGAGGAGTATTAAGATACGAGCGGTTTCCCTCGGAGCTCCCTCGTGGGCTC 643
Db |||||||
QY 644 TCCGTTCCGAGCGCTGCGCTTACCGGATACCTGTCGCGCTTTCTCCCTCGGAGCTC 1345
Db |||||||
QY 704 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCA 738
Db |||||||
QY 1406 GCGCTTTCTCATAGCTCACGCTGTAGGTATCTCA 1440

RESULT 5

US-09-347-311A-1
; Sequence 1, Application US/09347311A
; GENERAL INFORMATION:
; APPLICANT: Plaetnick, Geert
; APPLICANT: Plattewu, Christ
; APPLICANT: Mortier, Katharine
; APPLICANT: Bogaert, Thierry
; TITLE OF INVENTION: Characterisation of Gene Function using dsRNA
; FILE REFERENCE: D0590/7003
; CURRENT APPLICATION NUMBER: US/09/347,311A
; EARLIER FILING DATE: 1999-07-02
; EARLIER FILING DATE: 1998-07-03
; EARLIER FILING DATE: 1998-07-03
; EARLIER FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1

; TITLE OF INVENTION: Characterisation of Gene Function using dsRNA
; TITLE OF INVENTION: Inhibition
; FILE REFERENCE: D0590/7003
; CURRENT APPLICATION NUMBER: US/10/057,108
; CURRENT FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: 09/347,311
; PRIOR FILING DATE: 2001-01-04
; PRIOR APPLICATION NUMBER: GB 9814536.0
; PRIOR FILING DATE: 1998-07-03
; PRIOR APPLICATION NUMBER: GB 9827152.1
; PRIOR FILING DATE: 1998-12-09
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3216
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid DNA
; US-10-057-108-1

Query Match 93.7%; Score 691.8; DB 17; Length 3216;
Best Local Similarity 96.2%; Pred. No. 9.8e-192;
Matches 726; Conservative 0; Mismatches 12; Indels 17; Gaps 1;
QY 1 ATACGACTCAGTATAGGGCGAAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGACCT 60
Db 686 atagactcactatagggcggaattcgagctcggtacccggggtcctctagagtcggaag 745
QY 61 GCAGGC-----ATGCAAGCTTGAGTATCTATAGTGTACCTTAAATAG 103
Db 746 ctctcgccctatagtgagtcgtattacagcttgattctctatagtcacctaataag 805
QY 104 CTTGGCGTAAATCATGTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCACAATTC 163
Db 806 ctggtggaatcatagggcgaattcgagctcggtacccggggtcctctagagtcggaag 865
QY 164 ACACAAATACGAGCGGAAAGCATATAAGTGTAAAGCTTGGGGTGCCTTAATCAGTCAGCTA 223
Db 866 acacaacatacagcggaagcataaagtgtaaagcctgggtgcttaataagtcagtcgga 925
QY 224 ACTCAGATTAATTCGCTGCTCAGTCCGCTTTCAGTCCGGAACCTGTCTGTGCA 283
Db 926 actcacattaatgctgctgctcactgctgctgctgctgctgctgctgctgctgctgct 985
QY 284 GCTGATTAATGAATCGGCCAACCGGAGGAGGCGGTTTGGCTATTTGGCGCTCTTC 343
Db 1046 cgtctctcgtcactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1105
QY 404 TCACCTCAAGGGGTAATACGCTTATCCACAGAAATCAGGGGATAACGCGAGGAAACAT 463
Db 1106 tcaactcaaaagcgtaataacagttatccacagaatcaggggataacgcagggaaagacat 1165
QY 464 GTGAGCAAAAGCGCAGCAAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 523
Db 1166 gtgagcaaaagcgcaaaagggcggaacccgtataaaagggcggtggtggtggtggtggt 1225
QY 524 CCATAGGCTCGCCCGCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCG 583
Db 1226 cgtatggctcgc 1285
QY 584 AAACCCGACAGGACTATAAGATACAGCGGTTTCCCGCTTCCCGCTTCCCGCTTCCCGCTC 643
Db 1286 aaacccgacagactataaagataccagcggttcccccctggagctccctcgtgagctc 1345
QY 644 TCTGTTCGACCCCTCGCGTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAGCGT 703
Db 1346 tctgttccgacctgcccgttaccggtatccctgtccgctcttctcccttccggaagcgt 1405
QY 704 GCGGCTTCTCATAGCTACGCTGTAGGTATCTCA 738
Db 1406 ggcgcttctcatagctcagcgctgtaggtatctca 1440

RESULT 6
US-10-057-108-1
; Sequence 1, Application US/10057108
; GENERAL INFORMATION:
; APPLICANT: Plaeintek, Geert
; APPLICANT: Plaeintek, Christ
; APPLICANT: Mortier, Katharine
; APPLICANT: Bogaert, Thierry

Query Match 93.7%; Score 691.8; DB 37; Length 3216;
Best Local Similarity 96.2%; Pred. No. 9.8e-192;
Matches 726; Conservative 0; Mismatches 12; Indels 17; Gaps 1;

QY 1 ATACGACTCAGTATAGGGCGAAATTCGAGCTCGGTACCGGGGATCCTCTAGAGTCGACCT 60
Db 686 atagactcactatagggcggaattcgagctcggtacccggggtcctctagagtcggaag 745
QY 61 GCAGGC-----ATGCAAGCTTGAGTATCTATAGTGTACCTTAAATAG 103
Db 746 ctctcgccctatagtgagtcgtattacagcttgattctctatagtcacctaataag 805
QY 104 CTTGGCGTAAATCATGTCATAGCTGTTTCTGTGTGAAATGTTATCCGCTCACAATTC 163
Db 806 ctggtggaatcatagggcgaattcgagctcggtacccggggtcctctagagtcggaag 865
QY 164 ACACAAATACGAGCGGAAAGCATATAAGTGTAAAGCTTGGGGTGCCTTAATCAGTCAGCTA 223
Db 866 acacaacatacagcggaagcataaagtgtaaagcctgggtgcttaataagtcagtcgga 925
QY 224 ACTCAGATTAATTCGCTGCTCAGTCCGCTTTCAGTCCGGAACCTGTCTGTGCA 283
Db 926 actcacattaatgctgctgctcactgctgctgctgctgctgctgctgctgctgctgct 985
QY 284 GCTGATTAATGAATCGGCCAACCGGAGGAGGCGGTTTGGCTATTTGGCGCTCTTC 343
Db 986 gctgacttaataagtcgccaacgcgcgggagaggggttgggtatggggtgctctc 1045
QY 344 CGCTTCCTCGCTCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 403
Db 1046 cgtctctcgtcactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 1105
QY 404 TCACCTCAAGGGGTAATACGCTTATCCACAGAAATCAGGGGATAACGCGAGGAAACAT 463
Db 1106 tcaactcaaaagcgtaataacagttatccacagaatcaggggataacgcagggaaagacat 1165
QY 464 GTGAGCAAAAGCGCAGCAAAAGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 523
Db 1166 gtgagcaaaagcgcaaaagggcggaacccgtataaaagggcggtggtggtggtggtggt 1225
QY 524 CCATAGGCTCGCCCGCTGACGAGCATCACAAAATCGACGCTCAAGTCAGAGGTGGCG 583
Db 1226 cgtatggctcgc 1285
QY 584 AAACCCGACAGGACTATAAGATACAGCGGTTTCCCGCTTCCCGCTTCCCGCTTCCCGCTC 643
Db 1286 aaacccgacagactataaagataccagcggttcccccctggagctccctcgtgagctc 1345
QY 644 TCTGTTCGACCCCTCGCGTTACCGGATACCTGTCGCGCTTCTCCCTTCGGGAGCGT 703
Db 1346 tctgttccgacctgcccgttaccggtatccctgtccgctcttctcccttccggaagcgt 1405

QY 704 GCGCTTCTCATAGCTCAGCTGATGATCTCA 738
 Db 1406 ggcgtttctcatagctcaacgtgtggtatctca 1440

RESULT

US-09-539-698-2
 ; Sequence 2, Application US/09539698
 ; GENERAL INFORMATION:
 ; APPLICANT: GenStar Therapeutics Corporation
 ; APPLICANT: Alemany, Ramon
 ; APPLICANT: Fang, Xiangming
 ; APPLICANT: Zhang, Wei-Wei
 ; APPLICANT: Robert, Sobol
 ; TITLE OF INVENTION: Complementary-Adenoviral Vector System
 ; FILE REFERENCE: 97-087-B
 ; CURRENT APPLICATION NUMBER: US/09/539,698
 ; CURRENT FILING DATE: 2000-03-31
 ; PRIOR APPLICATION NUMBER: 08/797,160
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 4885
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)..(4885)
 ; OTHER INFORMATION: plasmid pGT8015
 ; NAME/KEY: misc_feature
 ; LOCATION: (148)..(933)
 ; OTHER INFORMATION: coding sequence (CDS) for human B7-1
 ; NAME/KEY: misc_feature
 ; LOCATION: (70)..(147)
 ; OTHER INFORMATION: coding sequence (CDS) for transmembrane protein B1 signal peptide
 ; NAME/KEY: rep_origin
 ; LOCATION: (1466)..(2049)
 ; OTHER INFORMATION: complement (1466..2049) / ColE1 origin
 ; NAME/KEY: misc_feature
 ; LOCATION: (3117)..(4244)
 ; OTHER INFORMATION: coding sequence (CDS) for Kanamycin resistance in 4244..3117 orle
 ; NAME/KEY: misc_feature
 ; LOCATION: (2239)..(3099)
 ; OTHER INFORMATION: coding sequence for ampicillin resistance in 3099..2239 orientat
 ; NAME/KEY: rep_origin
 ; LOCATION: (4245)..(4659)
 ; OTHER INFORMATION: complement (4245-4659) / P1 origin
 ; US-09-539-698-2

Query Match 90.8%; Score 669.8; DB 20; Length 4885;
 Best Local Similarity 95.68; Pred No. 3.2e-185;
 Matches 689; Conservative 0; Mismatches 32; Indels 0; Gaps 0;
 QY 18 GCGAATTCAGCTCGGTACCGGGGATCCTCTAGAGTCGACCTGCAGGCGATGCAAGCTTG 77
 Db 961 gcacacggcgccgttactagtggatccgagctcgggtaccagcttgatgcatgcttg 1020
 QY 78 AGTATTCTATAGTGTCACTAAATAGCTTGGCGTAATCATGTCATAGCTGTTCTCTGTG 137
 Db 1021 agtattctatagtctacctaataagcttggcgtaatactggtcatagctgttctcgtg 1080
 QY 138 TGAATTTGTTATCGGCTCACAAATTCACACATAGCAGCGGGAAGCATAAAGTGTA 197
 Db 1081 tgaattgttatcgcgtccaaattccacacacatagcagcggaagcataaagtgtaaa 1140
 QY 198 GCCTGGGGTGCCTAAATGAGTGAGTCACTACATTAATTTGGTTCGCTCACTGCCCGCT 257
 Db 1141 gcttgggtgctcaatagtgagctaaactcacattaatgctgtgctcactgcccgt 1200

QY 258 TTCCAGTCGGGAACCTGTGTCGACGTCATTAATGAATCGGCCAACGCCGGGAGA 317
 Db 1201 ttccagtcgggaacacctgtgtccagctgcatctaaatgaatcggcccaacgcggggaga 1260
 QY 318 GCGCGTTTGGGTATTGGGCGCTCTTCGCGTTCCTCGCTCACTGACTCGCTCGCTCGCTC 377
 Db 1261 ggcgggttgcgtattggcgctcttcgcttctcgtcgtcactgactgctgctcgctc 1320
 QY 378 GTTCGGCTCGCGGACGCGGTATCAGCTCACTCAAGCGCGGTAAATACGGTTATCCACAGAA 437
 Db 1321 gttcggctcgcgagcggtatcagctcactcaaaagcggtgaatacggtttaccacaga 1380
 QY 438 TCAGGGGATAACGACGAGGAAGAACATGTGAGCAAAAGCGCAGCAAGGCGGAGAACCGT 497
 Db 1381 tcaggggataacgcaggaagaacatgtgagcaaaagcgcaaaagcccggaaccgt 1440
 QY 498 AAAAAAGCGCGCTTGTGCGCTTTTTCATAGCTCCGCCCTCCGCTGACGAGCATCAAAA 557
 Db 1441 aaaaagcgcgctgtgctgctgctgttttccataggtcgcgcctcgcgcctgacgagcatcaaa 1500
 QY 558 AATCAGCGCTCAAGTCAGAGGTGGGAAACCGACAGGACTATAAAGATACCGAGCGT 617
 Db 1501 aatcagcgctcaagtcagaggtggcgaaacccgacaggaactataagataccagggcgttt 1560
 QY 618 CCCCTGGAAGCTCCCTCGCTGCTCTCTGTTCGACCTGCCGCTTACCGGATACCTG 677
 Db 1561 cccctggagctccctcgtgctcctctgttcgacactgctcgcctgtaccggatacctg 1620
 QY 678 TCCGCCCTTCTCCCTTCCGGAAGCGTGGCGCTTCTCATAGCTCAGCTGTTAGGTATCTC 737
 Db 1621 tccgcttctcccttcgggaagcggtggcgcttctcctatagctcagctcgtgtaggtatctc 1680
 QY 738 A 738
 Db 1681 a 1681

RESULT 8
 ; US-09-068-821-17
 ; Sequence 17, Application US/09068821
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: Method of quantifying tumour
 ; TITLE OF INVENTION: cells in a body fluid and a suitable test kit
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Brown, Martin, Haller & McClain
 ; STREET: 1660 Union Street
 ; CITY: San Diego
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 92101-2926
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PADAT Sequenzmodul Version 1.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/068,821
 ; FILING DATE:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: DE 195 42 795.5
 ; FILING DATE: 16-NOV-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 7249-1501
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (619)238-0999
 ; TELEFAX: (619)238-0062
 ; INFORMATION FOR SEQ ID NO: 17:
 ; SEQUENCE CHARACTERISTICS:


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Db 1482 GTGGCGAAACCCGACAGGACTATAAAGATACCAAGGCGTTTCCCCCTCGAAAGCTCCCTCGT 1541
Qy 638 GCGCTCTCCTGTTCGACACCTGCGCTTACCGGATACCTGTCCGCGCTTTCTCCCTTCGGG 697
Db 1542 GCGCTCTCCTGTTCGACACCTGCGCTTACCGGATACCTGTCCGCGCTTTCTCCCTTCGGG 1601
Qy 698 AAGCGTGGCGCTTCTCATAGCTCAGCGTGTAGGTATCTCA 738
Db 1602 AAGCGTGGCGCTTCTCATAGCTCAGCGTGTAGGTATCTCA 1642

RESULT 10
PCT-US94-10146-1
: Sequence 1, Application PC/TUS9410146
: GENERAL INFORMATION:
: APPLICANT:
: TITLE OF INVENTION: Intron Mediated Recombinant Techniques and
: NUMBER OF SEQUENCES: 3
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: ASCII (text)
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: PCT/US94/10146
: FILING DATE: 12-SEPT-1994
: CLASSIFICATION:
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4539 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: both
: MOLECULE TYPE: other nucleic acid
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 969..1259
: OTHER INFORMATION: /product= "E3 exon"
: FEATURE:
: NAME/KEY: misc_feature
: LOCATION: 1290..1559
: OTHER INFORMATION: /product= "E5 exon"
: PCT-US94-10146-1

Query Match 90.5%; Score 667.8; DB 1; Length 4539;
Best Local Similarity 97.9%; Pred. No. 1.2e-184;
Matches 688; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

Qy 39 GGGGATCCTCTAGAGTCGACCTCGACGCGATGCAAGCTTGAGTATTCTATAGTGCACCTA 98
Db 2235 GGGGATCCTCTAGAGTCGACCTCGACGCGATGCAAGCTTTTGTTCCTTTAGTGAGGGTTA 2294
Qy 99 AAT---AGCTTGGCGTAATCATGGTCATAGCTGTTCCCTGTGTGAAATTTGTAATCCGCTC 155
Db 2295 ATTTCGAGCTTGGCGTAATCATGGTCATAGCTGTTCCCTGTGTGAAATTTGTAATCCGCTC 2354
Qy 156 ACAATTCCACACACATACGAGCCGGAAGCATAAAGTGAAGCCCTGGGCTGCTAATGA 215
Db 2355 ACAATTCCACACACATACGAGCCGGAAGCATAAAGTGAAGCCCTGGGCTGCTAATGA 2414
Qy 216 GTGAGCTAACTCACATTAATTCGGTTGCCCTCACTCCCGCTTTCCAGTCGGGAAACCTG 275
Db 2415 GTGAGCTAACTCACATTAATTCGGTTGCCCTCACTCCCGCTTTCCAGTCGGGAAACCTG 2474
Qy 276 TCGTGCCAGCTGCAATTAATCGAATCGGCCAACGCGGGGAGAGGCGGTTTGCGGTATTGGG 335
Db 2475 TCGTGCCAGCTGCAATTAATCGAATCGGCCAACGCGGGGAGAGGCGGTTTGCGGTATTGGG 2534
Qy 336 CGCTCTTCGGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGGCGAGCG 395
Db 2535 CGCTCTTCGGCTTCCTCGCTCACTGACTCGCTGCGCTCGGTTCGGCTGCGGCGAGCG 2594

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/114,835
;   FILING DATE: 14-JUL-1998
;   ATTORNEY/AGENT INFORMATION:
;     NAME: Vincent, Matthew P.
;     REGISTRATION NUMBER: 36,709
;     REFERENCE/DOCKET NUMBER: HUV-008.03
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (617) 832-1000
;   TELEFAX: (617) 832-7000
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 4539 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
; MOLECULE TYPE: other nucleic acid
; TOPOLOGY: both
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 969..1259
; OTHER INFORMATION: /product= "E3 exon"
;
; FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: 1290..1559
; OTHER INFORMATION: /product= "E5 exon"
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; US-09-114-835-1
;
Query Match      90.5%; Score 667.8; DB 15; Length 4539;
Best Local Similarity 97.9%; Pred. No. 1.2e-184;
Matches 688; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 39 GGGGATCCTCTAGAGTCGACCTGCAGCGCATGCAAGCTTTCAGTATTCTATAGTGTCACCTA 98
Db 2235 GGGGATCCTCTAGAGTCGACCTGCAGCGCATGCAAGCTTTCAGTATTCTATAGTGAGGTGA 2294

QY 99 AAT---AGCTTGGCGTAATCATGTCATAGCTTTCCCTGTGTGAAATTTGTTATCCGCTC 155
Db 2295 ATTCGAGCTTGGCGTAATCATGTCATAGCTTTCCCTGTGTGAAATTTGTTATCCGCTC 2354

QY 156 ACAATTCACACAACATACGAGCGGGAAGCATAAAGCTGTAAGCTGGGTGCTCAATGA 215
Db 2355 ACAATTCACACAACATACGAGCGGGAAGCATAAAGCTGTAAGCTGGGTGCTCAATGA 2414

QY 216 GTGACTTAACCTCACATTAATTTGCGTTTGCCTCACTGCCCGCTTTCAGTCGGGAACCTG 275
Db 2415 GTGACTTAACCTCACATTAATTTGCGTTTGCCTCACTGCCCGCTTTCAGTCGGGAACCTG 2474

QY 276 TCGTGCCAGCTGCATTAATGAATCGGCCAACGCGGGGAGAGCGGTTTTGCCGTATTGGG 335
Db 2475 TCGTGCCAGCTGCATTAATGAATCGGCCAACGCGGGGAGAGCGGTTTTGCCGTATTGGG 2534

QY 336 CGCTCTTCGGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCG 395
Db 2535 CGCTCTTCGGCTTCCTCGCTCACTGACTCGCTCGCTCGCTCGCTCGCTCGCTCGCTCGCG 2594

QY 396 GTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGA 455
Db 2655 GTATCAGCTCACTCAAAGCGGTAATACGGTTATCCACAGAATCAGGGGATAACGCAGGA 2654

QY 516 GCSTTTTTCATAGGCTCCGCCCTTCAGGACATCAAAAAATTCAGCGCTCAAGTCAG 575
Db 2715 GCSTTTTTCATAGGCTCCGCCCTTCAGGACATCAAAAAATTCAGCGCTCAAGTCAG 2774

QY 576 AGGTGGCGAAACCAGCAGGACTATTAAGATACAGCGGTTTTCCCCTCGAAGCTCCCTC 635
Db 2775 AGGTGGCGAAACCAGCAGGACTATTAAGATACAGCGGTTTTCCCCTCGAAGCTCCCTC 2834

;
; RESULT 12
; US-09-114-835-1
; Sequence 1, Application US/09114835
; GENERAL INFORMATION:
; APPLICANT: Jarrell, Kevin A.
; TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES
; TITLE OF INVENTION: AND REAGENTS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley, Hoag & Eliot
; STREET: One Post Office Square
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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QY 636 GTGGCTCTCTGTTCCGACCTGCCGCTTACCGATACCTGTCGCCCTTTCTCCCTCCG 695
Db 2835 GTGGCTCTCTGTTCCGACCTGCCGCTTACCGATACCTGTCGCCCTTTCTCCCTCCG 2894
QY 696 GGAAGCCTGGCGCTTTCTCATAGTCACGCTGAGGTATCTCA 738
Db 2895 GGAAGCCTGGCGCTTTCTCATAGTCACGCTGAGGTATCTCA 2937

RESULT 13

US-09-399-593A-13
; Sequence 13, Application US/09399593A
; GENERAL INFORMATION:
; APPLICANT: Jarrell Ph.D., Kevin A
; APPLICANT: Mikheeva, Svetlana
; APPLICANT: Donahue, William
; TITLE OF INVENTION: INTRON-MEDIATED RECOMBINANT TECHNIQUES AND REAGENTS
; FILE REFERENCE: Ribozyme shuffling; improvments, in vivo
; CURRENT APPLICATION NUMBER: US/09/399,593A
; CURRENT FILING DATE: 1999-09-20
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 4542
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pIN1 plasmid
US-09-399-593A-13

Query Match 90.5%; Score 667.8; DB 17; Length 4542;
Best Local Similarity 97.9%; Pred. No. 1.2e-184;
Matches 688; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 39 GGGGATCCTCTAGAGTCGACCTGCAGGATGCAAGCTTGTAGTATCTATAGTGCACCTA 98
Db 2238 ggggattcctctagagtcgacctgcagcatgcaagctttgttccctttagtggaggtta 2297
QY 99 AAT---AGCTTGGCGTAATCATGTGTATAGTGTTCCTGTGTGCAAAATGTTATCCGCTC 155
Db 2298 atttcgagcttggcgaatacatggtcatagctgttctctgtggaattgtatccgctc 2357
QY 156 ACAATTCACACATACAGCGCGGAGGATGAAGTGAAGCTTGGGTGCTAATGA 215
Db 2358 acaattccacacatacagcgcggaagcataaagtgtaaagcctggggtgcctaata 2417
QY 216 GTGAGCTAACTACATTAATTTGGTTCGCTCACTGCGCTCACTGCGCTTCCAGTCGGGAACCTG 275
Db 2418 gtgagctaaactacattaatgttgctcaactgctcactgcttccagtcgggaacctg 2477
QY 276 TCGTGCACTGCATTAATTCGCCCAACGCGCGGGAGAGCGGTTTGCCTATTGGG 335
Db 2478 tcgtgccaactgcattaatgaaatcgcccaacgcgcgggagagcggtttgcgtattggg 2537
QY 336 CGCTCTCCGCTTCCTCGCTCACTCACTCGCTGCGCTCGCTGCTCGGCTGGCGAGCG 395
Db 2538 cgcctctccgcttccctcgctcaactgactgctgctcgctcgctcgctcgctcgctcgct 2597
QY 396 GTATCAGCTCACTCAAGCGCGTAATACGGTTATCCAGAAATCAGGGGATACGACGGA 455
Db 2598 gtatcagctcaactcaagcggttaatacggttatccagaaatcaggggataacgacgga 2657
QY 456 AAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCGGACCGTAAAGCGCGCTGCTG 515
Db 2658 aagaacatgtgagcaaaagcgacgaaagcgaaagcgaaagcgaaagcgaaagcgaaagcg 2717
QY 516 GCGTTTTCATAGCTCCGCCCTCGTACAGCATCACAAAATTCAGCGTCAAGTCAG 575
Db 2718 gcgctttccatagctccgccctcgctacagcatcacaaaatcagcggtcaagtcag 2777
QY 576 AGGTGGCAAAACCGCAGCAGCACTATAAAGATACCGAGCGTTTCCCTCGGAAGCTCCCTC 635

Db 2778 aggttgccgaaccccgacaggactataaagataccaggcgcttccccctggaagctccctc 2837
QY 636 GTGGCTCTCTGTTCCGACCTGCCGCTTACCGATACCTGTCGCCCTTTCTCCCTCCG 695
Db 2835 GTGGCTCTCTGTTCCGACCTGCCGCTTACCGATACCTGTCGCCCTTTCTCCCTCCG 2894
QY 696 GGAAGCCTGGCGCTTTCTCATAGTCACGCTGAGGTATCTCA 738
Db 2895 GGAAGCCTGGCGCTTTCTCATAGTCACGCTGAGGTATCTCA 2937

RESULT 14

US-09-724-624-93/c
; Sequence 93, Application US/09724624
; GENERAL INFORMATION:
; APPLICANT: Perera, Ranjan
; APPLICANT: Rice, Stephen
; APPLICANT: Eagleton, Clare
; APPLICANT: Lasham, Annette
; TITLE OF INVENTION: Compositions and Methods for the
; FILE REFERENCE: 11000.1036c3
; CURRENT APPLICATION NUMBER: US/09/724,624
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: U.S. No. 09/598,401
; PRIOR FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/NZ00/00018
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: U.S. No. 60/146,591
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: U.S. No. 09/276,599
; PRIOR FILING DATE: 1999-03-25
; NUMBER OF SEQ ID NOS: 130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 2571
; TYPE: DNA
; ORGANISM: Eucalyptus grandis
US-09-724-624-93

Query Match 90.4%; Score 667; DB 29; Length 2571;
Best Local Similarity 100.0%; Pred. No. 1.7e-184;
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 AGCTTGAGTATCTCATAGTGTACCTAAATAGCTTGGCGTAAATCATGCTCATAGCTGTT 131
Db 932 AGCTTGAGTATCTCATAGTGTACCTAAATAGCTTGGCGTAAATCATGCTCATAGCTGTT 873
QY 132 CCTGTGTGAATTTATTCGCTCACAAATCCACAAATACGAGCGGGAAGCATAAAG 191
Db 872 CCTGTGTGAATTTATTCGCTCACAAATCCACAAATACGAGCGGGAAGCATAAAG 813
QY 192 TGTAAAGCCTGGGTCGCTAATGAGTGAAGTAACTACATTAATTTGGCTGCTCACTG 251
Db 812 TGTAAAGCCTGGGTCGCTAATGAGTGAAGTAACTACATTAATTTGGCTGCTCACTG 753
QY 252 CCGCTTTCCAGTCGGGAAACCTGTGTGTCAGCTGATTAATGAATTCGCAACGCGG 311
Db 752 CCGCTTTCCAGTCGGGAAACCTGTGTGTCAGCTGATTAATGAATTCGCAACGCGG 693
QY 312 GGGAGAGCGGTTTGGCTATTGGGCGCTTTCGCTTCTCGCTCACTGCTGCTGCG 371
Db 692 GGGAGAGCGGTTTGGCTATTGGGCGCTTTCGCTTCTCGCTCACTGCTGCTGCG 633
QY 372 TCGGCTGTTTCGCTGCGGAGCGGTATCAGCTCACTCAAGCGGTAATACGCTTATCC 431
Db 632 TCGGCTGTTTCGCTGCGGAGCGGTATCAGCTCACTCAAGCGGTAATACGCTTATCC 573
QY 432 ACAGAAATCAGGGAATACCGCAGGAAAGACATGTGAGCAAAAGGCGCAAAAGGCGCAG 491
Db 572 ACAGAAATCAGGGAATACCGCAGGAAAGACATGTGAGCAAAAGGCGCAAAAGGCGCAG 513

us-10-014-743-3.rnpn

Thu Aug 1 12:08:50 2002

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OM nucleic - nucleic search, using sw model
Run on: August 1, 2002, 11:04:52 ; Search time 348.01 Seconds
(without alignments)
4595.698 Million cell updates/sec

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Gapop 10.0 , Gapext 1.0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	669.8	90.8	4885	US-09-539-698A-2	Sequence 2, Appli
2	667	90.4	2571	US-10-137-036-93	Sequence 93, Appl
3	667	90.4	3018	US-09-486-142-7	Sequence 7, Appli
4	667	90.4	3357	PCT-US02-17452-96	Sequence 96, Appl
5	667	90.4	3357	PCT-US02-17451-7	Sequence 7, Appli
6	667	90.4	3357	US-10-161-403-96	Sequence 96, Appl
7	667	90.4	3357	US-10-161-408-7	Sequence 7, Appli
8	666.8	90.4	8017	US-10-152-040-26	Sequence 26, Appl
9	666.8	90.4	8092	US-10-152-040-27	Sequence 27, Appl
10	666.8	90.4	10417	US-10-152-040-28	Sequence 28, Appl
11	665.8	90.2	6688	US-09-813-453A-72	Sequence 72, Appl
12	665.4	90.2	4606	PCT-US02-21336-27	Sequence 27, Appl
13	665.4	90.2	5983	PCT-US02-21336-30	Sequence 30, Appl
14	665.4	90.2	8320	US-09-813-453A-71	Sequence 71, Appl
15	645.8	87.5	2713	PCT-US02-17452-32	Sequence 32, Appl
16	645.8	87.5	2713	PCT-US02-17451-23	Sequence 23, Appl
17	645.8	87.5	2713	US-10-161-403-32	Sequence 32, Appl
18	645.8	87.5	2713	US-10-161-408-23	Sequence 23, Appl
19	638.2	86.5	7175	US-10-110-504-13	Sequence 13, Appl
20	638	86.4	3858	US-10-110-504-33	Sequence 33, Appl
21	638	86.4	4960	US-09-756-577-29	Sequence 29, Appl
22	638	86.4	5711	US-10-110-504-21	Sequence 21, Appl
23	638	86.4	7332	US-09-756-577-30	Sequence 30, Appl
24	637.6	86.4	8108	US-10-121-988-77	Sequence 77, Appl
25	637	86.3	3599	US-09-861-101B-3	Sequence 3, Appli

26	86.3	3600	5	US-09-861-101B-2	Sequence 2, Appli
27	86.3	3796	7	US-10-127-391-32	Sequence 32, Appl
28	86.3	4346	1	PCT-US02-17452-113	Sequence 113, Appl
29	86.3	4346	1	PCT-US02-17451-26	Sequence 26, Appl
30	86.3	4346	7	US-10-161-403-113	Sequence 113, Appl
31	86.3	4346	7	US-10-161-408-26	Sequence 26, Appl
32	86.3	4704	5	US-09-932-328-4	Sequence 4, Appli
33	86.3	5382	5	US-09-479-123-21	Sequence 21, Appl
34	86.3	5382	5	US-09-513-574-21	Sequence 21, Appl
35	86.3	5618	5	US-09-570-546-1	Sequence 1, Appli
36	86.3	5618	7	US-10-142-358-1	Sequence 1, Appli
37	86.3	6367	7	US-10-050-227-1	Sequence 2, Appli
38	86.3	6926	7	US-10-050-227-2	Sequence 2, Appli
39	86.3	7228	1	PCT-US02-15239-6	Sequence 6, Appli
40	86.3	7573	7	US-10-110-504-16	Sequence 16, Appl
41	86.3	7573	7	US-10-110-504-30	Sequence 30, Appl
42	86.3	8062	7	US-10-110-504-32	Sequence 32, Appl
43	86.3	8153	7	US-10-110-504-31	Sequence 31, Appl
44	86.3	8937	1	PCT-US02-17258-8	Sequence 8, Appli
45	86.3	8937	1	PCT-US02-17258-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1
US-09-539-698A-2
; Sequence 2, Application US/09539698A
; GENERAL INFORMATION:
; APPLICANT: GenStar Therapeutics Corporation
; APPLICANT: Alemany, Ramon
; APPLICANT: Fang, Xiangming
; APPLICANT: Zhang, Wei-Wei
; APPLICANT: Robert, Sobol
; TITLE OF INVENTION: Complementary-Adenoviral Vector System
; FILE REFERENCE: 97-087-B
; CURRENT APPLICATION NUMBER: US/09/539,698A
; CURRENT FILING DATE: 2000-03-31
; PRIOR FILING DATE: 1997-02-10
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 4885
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(4885)
; OTHER INFORMATION: plasmid pCT8015
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (148)..(933)
; OTHER INFORMATION: coding sequence (CDS) for human B7-1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (70)..(147)
; OTHER INFORMATION: coding sequence (CDS) for transmembrane protein B1 signal p
; FEATURE:
; NAME/KEY: rep_origin
; LOCATION: (1466)..(2049)
; OTHER INFORMATION: complement (1466..2049) / ColE1 origin
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3117)..(4244)
; OTHER INFORMATION: coding sequence (CDS) for kanamycin resistance in 4244..311
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22319)..(3099)
; OTHER INFORMATION: coding sequence for ampicillin resistance in 3099..2239 ori
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (22319)..(3099)
; OTHER INFORMATION: coding sequence for ampicillin resistance in 3099..2239 ori
; FEATURE:

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: NAME/KEY: rep_origin
: LOCATION: (4245)..(4659)
: OTHER INFORMATION: Complement (4245-4659) / Fl origin
US-09-539-698A-2

Query Match      90.8%; Score 669.8; DB 5; Length 4885;
Best Local Similarity 95.6%; Pred. No. 3.5e-185;
Matches 689; Conservative 0; Mismatches 32; Indels 0; Gaps 0;

QY 18 GCGAATTCGAGCTCGGTGATCCCGGGATCTCTAGAGTCAGCTGCAGGCATGCACGCTTG 77
Db 961 gcacatgggcgcttactagtgcagcagctcgggtaccaaggtgatgatcagcttg 1020
QY 78 AGTATTCTATAGTGCACCTAATAGCTTGGCGTAATCATGCTATAGCTGTTTCCTCTG 137
Db 1021 agtattctatagtcacctaataagcttggcgaatcatggtcatagctgttcccttg 1080
QY 138 TGAATATTGTTATCCGCTCACAAATCCACACAAACATACGAGCGGAGCATAAAGTGTAAA 197
Db 1081 tgaatattgttaccgctcacaaattccacacacatacagcgcgaagacataaagtgaaa 1140
QY 198 GCGTGGGTGGCTAATAGTGAAGCTAACTACATTTAATTCGCTTTCGCTCAGTGCCTGCT 257
Db 1141 gcttggggtgctaatgagtgagctaaactcaataattgcttgctgctcactgcgcct 1200
QY 258 TTCAGTTCGGGAACCTGCTGTCGAGTGCTAATTAATGAATCGGCCAACCGCGGGGAGA 317
Db 1201 ttcaagtgggaacacctgctgcaagctgcaataaagaaatgcgaacgcgcgggaga 1260
QY 318 GCGCGTTTGCCTATTGGCGCTCTTCGCTTCCTCGCTCACTGACTGCTGCGCTCGCTC 377
Db 1261 ggcggttgctattggcgctcttcgcttcctcgctcactgctgctgcgctcggtc 1320
QY 378 GTTCGCTGCGCGGAGCGGTATCAGCTCACTCAAGGCGGTAATACGGTTATCCACAGAA 437
Db 1321 gtgcgctggcgagcggtatcagctcactcaaaagcggaatacggttatccacagaa 1380
QY 438 TCAGGGGATAAGCGAGGAAAGACACTGAGCAAAAGGCGGACGCAAAAGGCCACGAGAACCT 497
Db 1381 tcaggggataacgcaggaagaaacaatgcagcaaaagggcgaagagccaggaacgct 1440
QY 498 AAAAGGCCGCGTTCGTGGCGTTTTCATPAGGCTCCGCGCCCTCAGCAGCATCACAAA 557
Db 1441 aaaaagccgcgtgtgctggcttttccataggtcgcgcgcctcgaagagagatcacaaa 1500
QY 558 AATCGACGCTCAAGTCAGAGTGGCGAAACCCGACAGGACTATAAGATACACAGCGTTT 617
Db 1501 aatcgacgctcaagtcagaggctggcaaacccgacaggaactaaagataccagcgctt 1560
QY 618 CCCCCGGAAGCTCCCTCGCTGCGCTCTCTGTTCCGACCCCTGCCGCTTACCGGATACCTG 677
Db 1561 cccctggagctccctcgctgcctctctggttcggaacctgcgcgttaacgcgatacctg 1620
QY 678 TCGCGCTTTCTCCCTTCGGGAAGCGTGGCGCTTCTCATAGCTACGCTGTAGGTATCTG 737
Db 1621 tcgcctttctcccttcgggaagcgtggcgctttctcatagctcacgctgtaggtatctc 1680
QY 738 A 738
Db 1681 a 1681

RESULT 2
US-10-137-036-93/c
: Sequence 93, Application US/10137036
: GENERAL INFORMATION:
: APPLICANT: Perera, Ranjan
: APPLICANT: Rice, Stephen
: APPLICANT: Bagleton, Claire
: APPLICANT: Lasham, Annette
: APPLICANT: Wood, Marion
: APPLICANT: Visser, Elizabeth

```

Db 669 gctttcccccctggaagctccctcgtcgtctcctcgtcgtccgacccgtccacgga 728
QY 672 TACCTGTCCGCTTCTCCTTCGGGAAGCOTGGCGCTTCTTCATAGCTACGCTGTAGG 731
Db 729 tacctgtccgcttctcctcctcgtggaagcgtggtcgttctcctcgtcgtcgtgtagg 788
QY 732 TATCTCA 738
Db 789 tatctca 795

RESULT 4

PCT-US02-17452-96
; Sequence 96, Application PC/TUS0217452
; GENERAL INFORMATION:
; APPLICANT: CHROMOS MOLECULAR SYSTEMS, INC.
; APPLICANT: Perkins, Edward
; APPLICANT: Perez, Carl
; APPLICANT: Lindenbaum, Michael
; APPLICANT: Greene, Amy
; APPLICANT: Leung, Josephine
; APPLICANT: Fleming, Elena
; APPLICANT: Stewart, Sandra
; APPLICANT: Shellard, Joan
; TITLE OF INVENTION: CHROMOSOME-BASED PLATFORMS
; FILE REFERENCE: 24601-420PC
; CURRENT APPLICATION NUMBER: PCT/US02/17452
; CURRENT FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/294,758
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: 60/366,891
; PRIOR FILING DATE: 2002-03-21
; NUMBER OF SEQ ID NOS: 129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 3357
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pGEMeasyNOS Plasmid
PCT-US02-17452-96

Query Match 90.4%; Score 667; DB 1; Length 3357;
Best Local Similarity 100.0%; Pred. No. 2.1e-184; Indels 0; Gaps 0;
Matches 667; Conservative 0; Mismatches 0;

QY 72 AGCTTGAGTATTCATAGTGTACCTAAATAGTGTGGCGTAATCATGTGTATAGCTGTTT 131
Db 70 agcttgagtattctatagtgctacacctaaatagcttggttaataatcgtcgtatgttt 129
QY 132 CTTGTGTGAATTTTATCCGCTCACAAATTCACACAAATACAGCGCGGAAGCATTAAG 191
Db 130 cctgtgtgaattgtttatccgctcacaaattccacacaaatcacgagccggaagcataag 189
QY 192 TGTAAAGCCCTGGGTGCTTAAATGAGTGTAGCTAATTAATTCCTGCTGCTGCTGCTG 251
Db 190 tgtaaagccctgggtgcttaataatgagctcaatccacataatgattgaatgagccacgcgcg 249
QY 252 CCCGCTTTCCAGTCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Db 250 cccgctttccagtcgggaacctgctgcccagctgctgctgctgctgctgctgctgctgctg 309
QY 312 GGGAGAGCGGTTTGGCTATTGGGGGCTTCTCCGCTTCTCGCTCAGCTGCTGCTGCTGCTG 371
Db 310 gggagagcggtttgctgattggcgctcctccgctcctccgctcctccgctcctccgctcct 369
QY 372 TCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431
Db 370 tccgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 429
QY 432 ACAGAAATCAGGGGATTAACGAGGAAAGAACATGTGTAGCAAAAGGCCACGAAAGGCCAGG 491

QY 732 TATCTCA 738
Db 272 TATCTCA 266

RESULT 3

US-09-486-142-7
; Sequence 7, Application US/09486142
; GENERAL INFORMATION:
; APPLICANT: Martinez, Jean
; APPLICANT: Goze, Catherine
; TITLE OF INVENTION: OLIGONUCLEOTIDES FOR IDENTIFYING PRECURSORS OF AMIDATED POLYPEPT
; TITLE OF INVENTION: HORMONES
; FILE REFERENCE: 427 034
; CURRENT APPLICATION NUMBER: US/09/486,142
; CURRENT FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: PCT/FR98/01767
; PRIOR FILING DATE: 1998-08-07
; PRIOR APPLICATION NUMBER: FR 97/10643
; PRIOR FILING DATE: 1997-08-26
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 3018
; TYPE: DNA
; ORGANISM: ARTIFICIAL SEQUENCE
; FEATURE:
; OTHER INFORMATION: VECTOR SEQUENCE: pGEM-T Easy Vector Plasmid Sequence
US-09-486-142-7

Query Match 90.4%; Score 667; DB 5; Length 3018;
Best Local Similarity 100.0%; Pred. No. 2.1e-184; Indels 0; Gaps 0;
Matches 667; Conservative 0; Mismatches 0;

QY 72 AGCTTGAGTATTCATAGTGTACCTAAATAGTGTGGCGTAATCATGTGTATAGCTGTTT 131
Db 129 agcttgagtattctatagtgctacacctaaatagcttggttaataatcgtcgtatgttt 188
QY 132 CTTGTGTGAATTTTATCCGCTCACAAATTCACACAAATACAGCGCGGAAGCATTAAG 191
Db 189 cctgtgtgaattgtttatccgctcacaaattccacacaaatcacgagccggaagcataag 248
QY 192 TGTAAAGCCCTGGGTGCTTAAATGAGTGTAGCTAATTAATTCCTGCTGCTGCTGCTGCTG 251
Db 249 tgtaaagccctgggtgcttaataatgagctcaatccacataatgctgctgctgctgctgctg 308
QY 252 CCCGCTTTCCAGTCGGGAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 311
Db 309 cccgctttccagtcgggaacctgctgcccagctgctgctgctgctgctgctgctgctgctg 368
QY 312 GGGAGAGCGGTTTGGCTATTGGGGGCTTCTCCGCTTCTCGCTCAGCTGCTGCTGCTGCTG 371
Db 369 gggagagcggtttgctgattggcgctcctccgctcctccgctcctccgctcctccgctcct 428
QY 372 TCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 431
Db 429 tcggtcgttcggtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtc 488
QY 432 ACAGAAATCAGGGGATTAACGAGGAAAGAACATGTGTAGCAAAAGGCCACGAAAGGCCAGG 491
Db 489 acagaatcagggataaacgaggaagaacatgtgagcaaaagccagcaaaagccagcagcag 548
QY 492 AACCGTAAAGCCGCTTGTGGCGTCTTCCATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 551
Db 549 aaccgtataaagccgctgt 608
QY 552 CACAAAAATCGAGCTCAAGTCAAGAGTGGCGAAACCCGAGAGCTATATAAGATACAC 611
Db 609 cacaataatcagcgtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcagtcag 668
QY 612 GCGTTTCCCCCTGGAAAGCTCCCTCGTGGCGCTCTCTCTGTTCCGAGCCCTGCGCTTACC 671

72	AGCTTGAGTATTCTATAGTGTCACTACCTAAATAGCTTGGCGTAATCAATGTCATAGCTGT	131
70	agcttgagtatcttatagtgctaccataatagcttgcgtaataatcatggtcgaagtgttt	129
132	CCGTGTGTGAATTTGTTATCCGCTCACAAATCCACACAAATACGAGCCGGAGCATAAAG	191
130	ccgtgtgaaattggttatccgctcacaattccacacaacatacagcggcgaagcataag	189
192	TGTTAAGCCTGGGGTGCCCTAATGAGTGAGCTAACTCACATTAAATTCGGTTGGCGTCACTG	251
190	tgtaagcctggggtgcctcaatgagtgcgtcaactcaataatgcttcgctcaactg	249
252	CCGGCTTTCCAGTCGGGAAACCTGTGTCGCCAGCTGCATTATGAATCGGCCAACCGCG	311
250	ccgctttccagtcgggaaacctgtgtgccagctgcgttaataatggaatcgccaacgcgcg	309
312	GGGAGAGCGGTTTCGGTATTGGCGGCTCTTCGGCTTCCTCGCTCACATGACTCGCTGGCG	371

	Query Match	90.4%	Score 667	DB 7	Length 3357
	Best Local Similarity	100.0%	Pred. No. 2.1e-184		
	Matches 667	Conservative 0	Mismatches 0	Indels 0	Gaps
QY	72	ACGTTTGAGCTATCTATAGTGCACCTAAATAGCTTGGCGTAATCAGTCATAGCTGTTTT	131		
Db	70	agcttgagattctatagtgctcaactcaaaatagcttcggtcaatcattcattgcatagctgttt	129		
QY	132	CGTGTGTGAATTTGTTATTCGCGCTCACAATTCACACAACTACGAGCGGAGCATTAAG	191		

Db	130	cctgtgtgaattgttatcgcgtccacaaattccacacatacagagccggaagcataaag	189
QY	192	TGTAAAGCCTGGGTGCTTAATGAGTGAAGTAACTACATTAATTTGGTTCGCTCACTG	251
Db	190	tgtaaagcctgggtgcttaagtgtgagctaaactcacataaattcggttgagctcaatg	249
QY	252	CCGCTTTCCAGTCGCGGAACCTGTGTCGAGCTGCATTAATGAATTCGCGCAACGCGCG	311
Db	250	cccgctttccagtcggaaacacctgtgctccagctgcatlaaagaaacggaacgagc	309
QY	312	GGAGAGCGGTTGGCTATTGGCGCTCTTCGCTTCCTCGCTCACTCGCTCGCG	371
Db	310	gggagagcggttggtattggcgctcttcgcttcctcgccactgactgctgctgcgc	369
QY	372	TGCGTTCGCTGCGGTGCGGAGCGGTATCAGCTCAAGGCGGTAATACGCTTATCC	431
Db	370	tcggtcgctcgctcgcgagcggtatcagctcaacaaagcggtlaaagcgttatcc	429
QY	432	ACAGATCAGGGGATAACGAGGAAAGACATGTGAGCAAAAGCCGCAAAAGCCGAGG	491
Db	430	acagaatcaggggataaacgcaggaagacatgtgagcaaaagccgcaaaagggccag	489
QY	492	AACCGTAAAGCGCGGTTGCTGGGCTTTTCATAGCTCCGCGCCCTGACGAGCAT	551
Db	490	aacgtaaaagggcggtgtgctggtttttccatagctccgccccctgacgagcat	549
QY	552	CACAAAATCAGCGCTCAAGTCAGAGTGCGGAAACCGCAGAGACTATAAAGATACCAG	611
Db	550	cacaaaatcagcgctcaagtcagaggtggcgaacccgagagactataaagataccag	609
QY	612	CGCTTCCCTCGAGCTCCCTCGTGCCTCTCTGTCGAGCTTCATAGCTACGCTGTAGG	671
Db	610	gcgttccctcggaagctccctcgctgctctctctgctccgacccctgacgctgtagg	729
QY	732	TATCTCA 738	
Db	730	tatctca 736	
RESULT 7			
US-10-161-408-7			
; Sequence 7, Application US/10161408			
; GENERAL INFORMATION:			
; APPLICANT: Perez, Carl			
; APPLICANT: Fabijanski, Steven			
; APPLICANT: Perkins, Edward			
; TITLE OF INVENTION: Plant Artificial Chromosomes, Uses thereof, and Methods of Prepa			
; FILE REFERENCE: 24601-419			
; CURRENT APPLICATION NUMBER: US/10/161,408			
; PRIOR FILING DATE: 2002-05-30			
; PRIOR FILING DATE: 2001-05-30			
; PRIOR APPLICATION NUMBER: US 60/294,687			
; PRIOR FILING DATE: 2001-05-30			
; NUMBER OF SEQ ID NOS: 51			
; SOFTWARE: FASTSEQ for Windows Version 4.0			
; SEQ ID NO 7			
; LENGTH: 3357			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			
; OTHER INFORMATION: pGEMEasyNOS Plasmid			
US-10-161-408-7			
Query Match 90.4%; Score 667; DB 7; Length 3357;			
Best Local Similarity 100.0%; Pred. No. 2,1e-184;			
Matches 667; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			

QY	72	AGCTTGAGTATTCCTATAGTGTCACTAAATAGCTTGGCGTAAATCATGTGCTATAGCTGTT	131
Db	70	agcttgagatctccatagctgcaacctaaatagcttgagcaataatgctcatagctgtt	129
QY	132	CCTGTGTAATTTGTTATTCGCTCAAAATCCACACACATACGAGCCGGAAGCATAAAG	191
Db	130	cctgtgtaattgttatccgctcaaatccacacacatacagagccggaagcataaag	189
QY	192	TGTAAGCCTGGGTGCTTAATGAGTGAAGTAACTACATTAATTTGGTTCGCTCACTG	251
Db	190	tgtaaagcctgggtgcttaagtgtgagctaaactcacataaattcggttgagctcaatg	249
QY	252	CCGCTTTCCAGTCGCGGAACCTGTGTCGAGCTGCATTAATGAATTCGCGCAACGCGCG	311
Db	250	cccgctttccagtcggaaacacctgtgctccagctgcatlaaagaaacggaacgagc	309
QY	312	GGAGAGCGGTTGGCTATTGGCGCTCTTCGCTTCCTCGCTCACTCGCTCGCG	371
Db	310	gggagagcggttggtattggcgctcttcgcttcctcgccactgactgctgctgcgc	369
QY	372	TGCGTTCGCTGCGGTGCGGAGCGGTATCAGCTCAAGGCGGTAATACGCTTATCC	431
Db	370	tcggtcgctcgctcgcgagcggtatcagctcaacaaagcggtlaaagcgttatcc	429
QY	432	ACAGATCAGGGGATAACGAGGAAAGACATGTGAGCAAAAGCCGCAAAAGCCGAGG	491
Db	430	acagaatcaggggataaacgcaggaagacatgtgagcaaaagccgcaaaagggccag	489
QY	492	AACCGTAAAGCGCGGTTGCTGGGCTTTTCATAGCTCCGCGCCCTGACGAGCAT	551
Db	490	aacgtaaaagggcggtgtgctggtttttccatagctccgccccctgacgagcat	549
QY	552	CACAAAATCAGCGCTCAAGTCAGAGTGCGGAAACCGCAGAGACTATAAAGATACCAG	611
Db	550	cacaaaatcagcgctcaagtcagaggtggcgaacccgagagactataaagataccag	609
QY	612	CGCTTCCCTCGAGCTCCCTCGTGCCTCTCTGTCGAGCTTCATAGCTACGCTGTAGG	671
Db	610	gcgttccctcggaagctccctcgctgctctctctgctccgacccctgacgctgtagg	729
QY	672	TACCTGTCCGCTTTCTCCCTTCGCGGAAGCGTGGCGCTTTCTCATAGCTACGCTGTAGG	731
Db	670	tacctgtccgctttctcccttcggaagcggtggcgctttctcatagctcagctgtagg	729
QY	732	TATCTCA 738	
Db	730	tatctca 736	
RESULT 8			
US-10-152-040-26			
; Sequence 26, Application US/10152040			
; GENERAL INFORMATION:			
; APPLICANT: ESCRIOU, NICOLAS			
; APPLICANT: VAN DER WERF, SYLVIE			
; APPLICANT: VIGNUZZI, MARCO			
; APPLICANT: GERBAUD, SYLVIE			
; TITLE OF INVENTION: REPLICONS DERIVED FROM POSITIVE STRAND RNA VIRUS			
; TITLE OF INVENTION: GENOMES USEFUL FOR THE PRODUCTION OF HETEROLOGOUS			
; FILE REFERENCE: 03495.0229-00000			
; CURRENT APPLICATION NUMBER: US/10/152,040			
; CURRENT FILING DATE: 2002-06-27			
; PRIOR APPLICATION NUMBER: 60/292,515			
; PRIOR FILING DATE: 2001-05-23			
; NUMBER OF SEQ ID NOS: 28			
; SOFTWARE: PatentIn Ver. 2.1			
; SEQ ID NO 26			
; LENGTH: 8017			
; TYPE: DNA			
; ORGANISM: Artificial Sequence			
; FEATURE:			

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: plasmid pm(DELTA)BB
US-10-152-040-26

Query Match 90.4%; Score 666.8; DB 7; Length 8017;
Best Local Similarity 97.9%; Pred. No. 3e-184;
Matches 687; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 40 GGGATCTCTAGAGTCGACCTGCAGCGCATGCAAGCTTGAGTATTCTATAGTCTCACTAA 99
DB 4836 gggatctcttagagtcgacctgcaggcatgcaagctttgttcccttttagtgagggttaa 4895
QY 100 AT---AGCTTGGGTAATCATAGCTGTTTCTCTGTGTAATTTCTATCGCTCA 156
DB 4896 ttccgagcttggtgtaataatcatagctgttccctgtgtaaatgtttatccgctca 4955
QY 157 CAATTCCACACACATACGAGCGGGAAGATGTAAGCTTGGGGTGCCCTAATGAG 216
DB 4956 caattccacacacatacagagccggaagcaaaaagtgtaagcctggggtccctaatgag 5015
QY 217 TGAGCTAACTCACATTAATTCGCTGCTCACTGCCGCTTTCAGTCGGGAAACCTGT 276
DB 5016 tgagctaactcacattaatgctgtgctcaactgcccgtttccagtccgggaacacctgt 5075
QY 277 CGTGCCAGCTGCATTAATGATCGGCCAAGCGCGGGGAGGCGGTTTGGGTATTTGGGC 336
DB 5076 cgtgcagctgcattatgaatcgcccaagcgcgaggagagcgggttgcgtattgggc 5135
QY 337 GCTCTTCCGCTTCCCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 396
DB 5136 gctcttccgcttccctcgctcaactgactcgctgctgctgctgctgctgctgctgctg 5195
QY 397 TATCAGCTCACTCAAAAGCGGTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 456
DB 5196 tatcagctcaactcaaaaggcgtaatacgggttatccacagaaatcagggaataacgcaggaa 5255
QY 457 AGAATGTCGACAAAAGCGCCAGCAAAAGCGCCAGCAAAAGCGCCAGCAAAAGCGCC 516
DB 5256 agaactgtgagcaaaaggccagcaaaaggccagcaaaaggccagcaaaaggccagcaaaagg 5315
QY 517 GCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAGA 576
DB 5316 cgttttccataggctccgccccctgacgagcatcacaaaatcagcgctcaagtcaga 5375
QY 577 GTGGCGAAACCCGACGAGCACTAATAAGATACAGCGCTTTCGCCCTGGAAGCTCCCTCG 636
DB 5376 ggtggcgaaacccgacaggaactataaagatacaggcggtttcccccctggagcctccctcg 5435
QY 637 TCGCTCTCCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTTCGG 696
DB 5436 tgcgctctcctgttccgacctgcccgttaccggataacctgtccgctttctcccttcgg 5495
QY 697 GAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCA 738
DB 5496 gaagcgtggcgcttctcatagctcaactcaactgtaggtatctca 5537

RESULT 9

US-10-152-040-27
; Sequence 27, Application US/10152040
; GENERAL INFORMATION:
; APPLICANT: ESCRIOU, NICOLAS
; APPLICANT: VAN DER WERF, SYLVIE
; APPLICANT: VIGNUZZI, MARCO
; APPLICANT: GERBAUD, SYLVIE
; TITLE OF INVENTION: REPLICONS DERIVED FROM POSITIVE STRAND RNA VIRUS
; TITLE OF INVENTION: GENOMES USEFUL FOR THE PRODUCTION OF HETEROLOGOUS
; FILE REFERENCE: 03495, 0229-00000
; CURRENT APPLICATION NUMBER: US/10/152,040
; CURRENT FILING DATE: 2002-06-27
; PRIOR APPLICATION NUMBER: 60/292,515

; PRIOR FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27

LENGTH: 8092
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: plasmid pm(DELTA)FM
US-10-152-040-27

Query Match 90.4%; Score 666.8; DB 7; Length 8092;
Best Local Similarity 97.9%; Pred. No. 3e-184;
Matches 687; Conservative 0; Mismatches 12; Indels 3; Gaps 1;

QY 40 GGGATCTCTAGAGTCGACCTGCAGCGCATGCAAGCTTGAGTATTCTATAGTCTCACTAA 99
DB 4911 gggatctcttagagtcgacctgcaggcatgcaagctttgttcccttttagtgagggttaa 4970
QY 100 AT---AGCTTGGGTAATCATAGCTGTTTCTCTGTGTAATTTCTATCGCTCA 156
DB 4971 ttccgagcttggtgtaataatcatagctgttccctgtgtaaatgtttatccgctca 5030
QY 157 CAATTCCACACACATACGAGCGGGAAGATGTAAGCTTGGGGTGCCCTAATGAG 216
DB 5031 caattccacacacatacagagccggaagcaaaaagtgtaagcctggggtccctaatgag 5090
QY 217 TGAGCTAACTCACATTAATTCGCTGCTCACTGCCGCTTTCAGTCGGGAAACCTGT 276
DB 5091 tgagctaactcacattaatgctgtgctcaactgcccgtttccagtcgggaacacctgt 5150
QY 277 CGTGCCAGCTGCATTAATGATCGGCCAAGCGCGGGGAGGCGGTTTGGGTATTTGGGC 336
DB 5151 cgtgcagctgcattatgaatcgcccaagcgcgaggagagcgggttgcgtattgggc 5210
QY 337 GCTCTTCCGCTTCCCTCGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 396
DB 5211 gctcttccgcttccctcgctcaactgactcgctgctgctgctgctgctgctgctgctg 5270
QY 397 TATCAGCTCACTCAAAAGCGGTAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 456
DB 5271 tatcagctcaactcaaaaggcgtaatacgggttatccacagaaatcagggaataacgcaggaa 5330
QY 457 AGAATGTCGACAAAAGCGCCAGCAAAAGCGCCAGCAAAAGCGCCAGCAAAAGCGCC 516
DB 5331 agaactgtgagcaaaaggccagcaaaaggccagcaaaaggccagcaaaaggccagcaaaagg 5390
QY 517 GCTTTTCCATAGGCTCCGCCCCCTGACGAGCATCACAAAATCAGCGCTCAAGTCAGA 576
DB 5391 cgttttccataggctccgccccctgacgagcatcacaaaatcagcgctcaagtcaga 5450
QY 577 GTGGCGAAACCCGACGAGCACTAATAAGATACAGCGCTTTCGCCCTGGAAGCTCCCTCG 636
DB 5451 ggtggcgaaacccgacaggaactataaagatacaggcggtttcccccctggagcctccctcg 5510
QY 637 TCGCTCTCCTGTTCCGACCTGCGCTTACCGGATACCTGTCCGCTTTCCTCCCTTCGG 696
DB 5511 tgcgctctcctgttccgacctgcccgttaccggataacctgtccgctttctcccttcgg 5570
QY 697 GAAGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCA 738
DB 5571 gaagcgtggcgcttctcatagctcaactcaactgtaggtatctca 5612

RESULT 10

US-10-152-040-28
; Sequence 28, Application US/10152040
; GENERAL INFORMATION:
; APPLICANT: ESCRIOU, NICOLAS
; APPLICANT: VAN DER WERF, SYLVIE
; APPLICANT: VIGNUZZI, MARCO

RESULT 11
US-09-813-453A-72
; Sequence 72, Application US/09813453A
; GENERAL INFORMATION:
; APPLICANT: Yocum, R. Rogers
; TITLE OF INVENTION: MICROORGANISMS AND ASSAYS FOR THE IDENTIFICATION OF
; TITLE OF INVENTION: ANTIBIOTICS
; FILE REFERENCE: OG2-001
; CURRENT APPLICATION NUMBER: US/09/813,453A
; CURRENT FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/227,860
; PRIOR FILING DATE: 2000-08-24
; PRIOR APPLICATION NUMBER: 09/667,569
; PRIOR FILING DATE: 2000-09-21
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 72
; LENGTH: 6688
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: plasmid, pAN336
; OTHER INFORMATION: Description of Artificial Sequence: plasmid, pAN336
US-09-813-453A-72

Query Match 90.4%; Score 666.8; DB 7; Length 10417;
Best Local Similarity 97.9%; Pred. No. 3.2e-184;
Matches 687; Conservative 0; Mismatches 12; Indels 3; Gaps 1;
US-10-152-040-28
QY 40 GGGATCCTCTAGAGTCGACCTGACGATCGAAGCTTGAGTATCTATAGTGTCACTTAA 99
Db 7236 gggatcctctagagtcgacgtcgagcatgcaagcttttttcccttagtgagggttaa 7295
QY 100 AT---AGCTTGGCTTAATCATGTGTATAGTGTTCCTGTGTGAATTTTATCCGCTCA 156
Db 7296 ttcgagcttggcgttaataatgctatgctttctctgtgtaattgttaccgctca 7355
QY 157 CAATTCCACACACATAGGACCGGAGCAGTAAAGCTTGAAGCTGGGGTGCCTAATGAG 216
Db 7356 caattccacacacatagagccggagcgttaaaagttaaaagctggggtgctaaatgag 7415
QY 217 TGAGTAACTCACATTAATTCGGTTCGCTCAGTGCCTGCTTCCAGTCGGGAACCTGT 276
Db 7416 tgagtaactcacattaatttcgctgctcactgctcctgcttccagtcgggaacclgt 7475
QY 277 CGTCCAGCTGATTAATGAATCGCCGACGCGGGGAGAGCGGTTTGGGTATTTGGGC 336
Db 7476 cgtgcagctgattaatgaatcgggccaacgcgcgggagagcggttttggtattgggc 7535
QY 337 GCTCTTCCGCTTCCCTCGCTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 396
Db 7536 gctcttccgcttccctcgctcactgactgctgctgctgctgctgctgctgctgctg 7595
QY 397 TATCAGCTCACTCAAGAGCGGTAAATACGGTTATCCACAGATCAGGGGATAACGAGGAA 456
Db 7596 tatcagctcactcaagaggggttaatacaggttatccacagatacaggggataacgagaa 7655
QY 457 AGAACATGTGAGCAAAAGGCCAGCAAAAGCCAGAACCGTAAAGCGCGCTTCTGCTGG 516
Db 7656 agaacatgtagcaaaagccagaaaagccaggaacgttaaaagggcgctgctgctg 7715
QY 517 CGTTTTCATAGCTCCGCGCCCTCAGCAGCATCAAAAATTCGACGCTCAAGTCAAGA 576
Db 7716 cgttttccataggtccgccccctgacgagcatcaaaaaatcgacgctcaagtcaga 7775
QY 577 GGTGCGAAACCCGACAGGACTATAAAGATACACAGGCGTTTCCCTTGGAGCTCCCTCG 636
Db 7776 ggttggcgaaacccgacaggaactataaagataccagggcgtttcccttggaaagctccctcg 7835
QY 637 TCGCTCTCTCTGTTCCGACCTCGCGCTTACCGGATACCTCTCGGCTTTTCTCCCTTGG 696
Db 7836 tgcgtctctctgttcgcagacctgcgcttaccgggatacgttcgcgttttctcccttcg 7895
QY 697 GAAGGCTGGCGCTTTCTCATAGCTCAGCTGTAGTATCTCA 738
Db 7896 gaagcgctggcgttttctcatagctcagcgtgtgaggtatctca 7937

Query Match 90.2%; Score 665.8; DB 5; Length 6688;
Best Local Similarity 98.2%; Pred. No. 5.6e-184;
Matches 673; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
US-09-813-453A-72
QY 54 TCGACCTGACGATCGAAGCTTGAGTATCTATAGTGTCACTTAATAGCTTGGCGTAA 113
Db 3981 tggacgcgttggatgcatagcttgagttattctctatagtcacctaataagctggcgtaa 4040
QY 114 TCATGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCCGCTCACATTCACACACATA 173
Db 4041 tcatggtcatagctgttctctgtgtaattgttatcgcgtcacaattccacacaacata 4100
QY 174 CGAGCCGGAAGCATAAAGTGTAAAGCTTGAAGCTTGAAGCTTGAAGCTTGAAGCTTGA 233
Db 4101 cgaagccggaagcaaaagtgtaaagcttccagtcgggaaacctgctgcccagtcacatta 4160
QY 234 ATTGCTGTGCGCTCAGTGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 293
Db 4161 attgctgtgctcactgctcctgcttccagtcgggaaacctgctgcccagtcacatta 4220
QY 294 TGAATCGGCCAACGCGCGGAGAGCGGTTTGGCTATTGGGCGCTCTTCCGCTTCTCTCG 353
Db 4221 tgaatcgcccaacgcgcggggagaggggttggctattggcgctcttccgcttccctcg 4280
QY 354 CTCACCTGACTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 413
Db 4281 ctcaactgactgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctg 4340
QY 414 GGGGTAAATACGTTATCCACAGATCAGGGGATAACGAGGAAACATGATGAGCAAAA 473
Db 4341 gcggttaacgggttaaccacagaaatcaggggataacgcaggaagaaatgtgagcaaa 4400
QY 474 GGCAGCAAAAGGCCAGGAACCGTAAAGCGCGCTTGGTGGCTTTTCCATAGGCTC 533
Db 4401 ggcagcaaaaagccaggaacccgttaaaagggcggttggctgctgcttcttcgataggctc 4460
QY 534 CGGCCCTCTGACGAGCATCAAAAATCGACGCTCAAGTTCAGAGGTGGCGAAACCGGACA 593
Db 4461 cgccccctgacgagcatcaaaaaatcgacgctcaagtcaagtgaggggtggcgaaacccgaca 4520
QY 594 GGACTATAAAGATACAGGCGGTTTCCCGCTGGAGCTCCCTCGTGGCTCTCTCTGTTCCG 653
Db 4521 ggaactataaagataccagggcggtttcccttggaaagctccctcgcgctctctctctcgcg 4580
QY 654 ACCCTGCGCGCTTACCGGATACCTGCTGCGCTTCTCTCCCTTCCGGAAGCGTGGCGCTTCT 713
Db 713 accctgcgcgcttaccggataccctgctgctgcttctctcccttccggaagcgctggcgcttctctcgcg

Db 4581 accctgcgctaccaggtacccgtccgcttctcccttctcccttctccggaagcgtggcgcttctct 4640
QY 714 CATAGCTCAGCTGTAGGTATCTCA 738
Db 4641 catagctcacgctgtagtatctca 4665
RESULT 12
PCT-US02-21336-27
; Sequence 27, Application PC/TUS0221336
; GENERAL INFORMATION:
; APPLICANT: OmniGene BioProducts, Inc. et al.
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154PC
; CURRENT APPLICATION NUMBER: PCT/US02/21336
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 27
; LENGTH: 4606
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
PCT-US02-21336-27

Query Match 90.2%; Score 665.4; DB 1; Length 4606;
Best Local Similarity 99.9%; Pred. No. 6.7e-184;
Matches 666; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 72 AGCTTGAGTATCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTCTATAGCTGTGT 131
Db 1917 agcttgagttattctatagtgtaacataatagcttggttaatactggtcatagctgtt 1976
QY 132 CCTGTGTAAATTTGTTATCCGCTCACAAATCCACAGAACATACGAGCCGGAAGCATAAAG 191
Db 1977 cctgtgtgaaattgttatccgctcacaaatccacacacatacagagcgggaagcataaag 2036
QY 192 TGTAAAGCCGTGGGTGCTTAATGAGTGAGCTAACTCACATTAATTCGTTTGGCTCAGTG 251
Db 2037 tgtaaagccctgggtgcttaagtgtgagctaaactcacatgaattggttggctcactg 2096
QY 252 CCGCTTTCCAGTCGGGAACCTGTGTCGACGCTGCATTAATGAATCGCCCAACCGCGG 311
Db 2097 ccgctttccagtcgggaacactgtctgcccagctgcatgaatgaatcgccaaagcgcg 2156
QY 312 GGGAGAGCGGTGTGCGTATTGGGCGCTCTTCCGCTTCTCGCTCAGTCACTGCTGCTGCG 371
Db 2157 gggagagcggtgttgcgtattggcgctcttccgcttctcgtcactgactcgctgcgc 2216
QY 372 TCGGTGCTTTCGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCC 431
Db 2217 tcggtcgttcggtcgcgagcggtatcagctcactcaaaagcggtgaatcggttacc 2276
QY 432 ACAGAAATCAGGGATTAACGCGAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGG 491
Db 2277 acagaatcaggggataacgcaggaaagaaacatgtgagcaaaagccagcaaaagggcgag 2336
QY 492 AACCGTAAAAAGGCCGCTTCTGCGCTTTTCCATAGGCTCCGCCCTCCCTGACGAGCAT 551
Db 2337 aaccgtaaaaagggcggtgtgctggcttttccgataggtccgccccctgacgagcat 2396
QY 552 CACAAAATCAGCGCTCAAGTCAGAGTGGCGAAACCCGACGAGCTATATAAGATACCAG 611
Db 2397 cacaaaatcagcgctcaagtcagaggtggcgaaacccgacagactataaagataccag 2456
QY 612 CGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCCTGTCGAGCTTCCCGCTTACCGGA 671
Db 2457 gctttcccccctggaagctccctcgctcctctctctctctctctctctctctctctctct 2516
QY 672 TACCTGTCCCGCTTCTCCCTTCGGGAAGGCTGGCGCTTCTCATAGCTCACGCTGTAGG 731

Db 2517 tacctgcgcttcttctcccttctccggaagcgtggcgcttctctcatagctcacgctgag 2576
QY 732 TATCTCA 738
Db 2577 tatctca 2583
RESULT 13
PCT-US02-21336-30
; Sequence 30, Application PC/TUS0221336
; GENERAL INFORMATION:
; APPLICANT: OmniGene BioProducts, Inc. et al.
; TITLE OF INVENTION: MICROORGANISMS AND PROCESSES FOR ENHANCED PRODUCTION OF
; FILE REFERENCE: BGI-154PC
; CURRENT APPLICATION NUMBER: PCT/US02/21336
; CURRENT FILING DATE: 2002-07-03
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 5983
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
PCT-US02-21336-30

Query Match 90.2%; Score 665.4; DB 1; Length 5983;
Best Local Similarity 99.9%; Pred. No. 7.1e-184;
Matches 666; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 72 AGCTTGAGTATCTATAGTGTACCTAAATAGCTTGGCGTAATCATGTCTATAGCTGTGT 131
Db 3294 agcttgagttattctatagtgtaacataatagcttggttgaatcattggtcatagctgtt 3353
QY 132 CCTGTGTAAATTTGTTATCCGCTCACAAATCCACAGAACATACGAGCCGGAAGCATAAAG 191
Db 3354 cctgtgtgaaattgttatccgctcacaaatccacacacatacagagcgggaagcataaag 3413
QY 192 TGTAAAGCCGTGGGTGCTTAATGAGTGAGCTAACTCACATTAATTCGTTTGGCTCAGTG 251
Db 3414 tgtaaagccctgggtgcttaagtgtgagctaaactcacatgaattggttggctcactg 3473
QY 252 CCGCTTTCCAGTCGGGAACCTGTGTCGACGCTGCATTAATGAATCGCCCAACCGCGG 311
Db 3474 ccgctttccagtcgggaacactgtctgcccagctgcatgaatgaatcgccaaagcgcg 3533
QY 312 GGGAGAGCGGTGTGCGTATTGGGCGCTCTTCCGCTTCTCGCTCAGTCACTGCTGCTGCG 371
Db 3534 gggagagcggtgttgcgtattggcgctcttccgcttctcgtcactgactcgctgcgc 3593
QY 372 TCGGTGCTTTCGCTGCGGCGAGCGGTATCAGCTCACTCAAGGCGGTAAATACGGTTATCC 431
Db 3594 tcggtcgttcggtcgcgagcggtatcagctcactcaaaagcggttaacaggttatcc 3653
QY 432 ACAGAAATCAGGGATTAACGCGAAGAACATGTGAGCAAAAGGCGCAGCAAAAGGCCAGG 491
Db 3654 acagaatcaggggataacgcaggaaagaaacatgtgagcaaaagggcgcaaaagggcgag 3713
QY 492 AACCGTAAAAAGGCCGCTTCTGCGCTTTTCCATAGGCTCCGCCCTCCCTGACGAGCAT 551
Db 3714 aaccgtaaaaagggcggtgtgctggcttttccgataggtccgccccctgacgagcat 3773
QY 552 CACAAAATCAGCGCTCAAGTCAGAGTGGCGAAACCCGACGAGCTATATAAGATACCAG 611
Db 3774 cacaaaatcagcgctcaagtcagaggtggcgaaacccgacagactataaagataccag 3833
QY 612 CGGTTTCCCGCTGGAAGCTCCCTCGTGGCTCTCCCTGTCGAGCTTCCCGCTTACCGGA 671
Db 3834 gctttcccccctggaagctccctcgctcctctctctctctctctctctctctctctctct 3893

Db 691 ggcgggttgctgattggcgctcttcgcgtcttcctcgtcactgactgctgcgtcgctc 750
 QY 378 GTTCGGCTGCGCGAGCGGTATCAGCTCACTCAAGGGGTAATACGGTTATCCACAGAA 437
 Db 751 gtteggctgcggcgagcgtatcagctcactcaaaagcggttaatacgtttatccacagaa 810
 QY 438 TCAGGGGATAACGCGAGGAAAGCAATGTGACCAAAAGGCCAGCAAAAGGCCAGGACCGT 497
 Db 811 tcaggggataacgcagcagaaagacatgtgagcaaaagccagcaaaagccaggaaccgt 870
 QY 498 AAAAGGCCGCGTTGCTGGGCTTTTTCATAGGCTCCGCCCTGACGAGCATCACAAA 557
 Db 871 aaaaagccgcgttgctggcgttttccataggtccgccccctgacgagcatcaca 930
 QY 558 AATCGACGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAAGATACCAAGCGT 617
 Db 931 aatcgacgtccaagtcagaggtggcgaaccgcagagactataaagataccagggcgtt 990
 QY 618 CCCCCTGGAAGCTCCCTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 677
 Db 991 cccctggaagctccctcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgtcgt 1050
 QY 678 TCCGCTTTTCTCCCTGCGGAGCGTGGCGCTTCTCATAGCTCAGGCTGTAGGTATGTC 737
 Db 1051 tcgcctttctccctcgggaagcgtggcgctttctcatagctcagctgtaggatctc 1110
 QY 738 A 738
 Db 1111 a 1111

Search completed: August 1, 2002, 11:05:27
 Job time: 8722 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 07:39:54 ; Search time 2881.61 Seconds

(*without alignments)

8837.974 Million cell updates/sec

Title: US-10-014-743-1

Perfect score: 1217

Sequence: 1 GCCACGTTGCTGCTGCA.....GGACAATTCTGGCCACACAGAG 1217

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0 *

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htgo_inv.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Match Length DB ID Description

1	1217	100.0	1217	6	AR036903	Sequence
2	1217	100.0	1217	6	ARI41142	Sequence
3	1215.4	99.9	7249	12	SYNM13M18	X025113 Cloning vec
4	1215.4	99.9	7250	12	SYNM13M18V	M77815 M13mpl8 pha
5	1201.2	98.7	64372	2	HSLOCAG	Z84493 Homo sapien
6	1184.8	97.4	7244	12	SYNM13M10V	L08819 M13mpl0 pha
7	1165.2	95.7	9955	6	I08051	I08051 Sequence 7
8	1161.4	95.4	7196	12	SYNM13M2V	L08818 M13mp2 phag
9	1161.4	95.4	7229	12	SYNM13M8V	M77826 M13mp8 phag
10	1161.4	95.4	7229	12	SYNM13M8V	M77826 M13mp8 phag
11	1161.4	95.4	7232	12	SYNM13M8V	M77826 M13mp8 phag
12	1161.4	95.4	7238	12	SYNM13M7V	M77689 M13mp8/pUC8
13	1161.4	95.4	7265	12	SYNM13M7V	M77689 M13mp8/pUC8
14	1159.8	95.3	7196	12	SYNM13M7V	M77689 M13mp8/pUC8
15	1156.8	95.1	7265	12	SYNM13M7V	M77689 M13mp8/pUC8
16	1156.4	95.0	7244	12	SYNM13M1V	L08833 M13mpl1 pha
17	1156.4	95.0	7250	12	SYNM13M1V	L08833 M13mpl1 pha
18	1156.4	95.0	7250	12	SYNM13M1V	L08833 M13mpl1 pha
19	1150.8	94.6	7294	6	ARI61799	L08874 Phagescript
20	1150.8	94.6	7294	6	ARI61799	L08874 Phagescript
21	1140.4	93.7	7083	6	ARI61803	ARI61803 Sequence
22	1131.4	93.0	7317	6	ARI61803	ARI61803 Sequence
23	1131.4	93.0	7317	6	ARI61803	ARI61803 Sequence
24	1131.4	93.0	7320	6	ARI61800	ARI61800 Sequence
25	1131.4	93.0	7557	6	AR035977	AR035977 Sequence
26	1131.4	93.0	7557	6	AR035977	AR035977 Sequence
27	1131.4	93.0	8118	6	AR035978	AR035978 Sequence
28	1131.4	93.0	8118	6	AR035978	AR035978 Sequence
29	1131.4	92.9	7394	6	ARI61804	ARI61804 Sequence
30	1131.4	92.9	7409	6	ARI61802	ARI61802 Sequence
31	1131.4	92.9	7445	6	AR035974	AR035974 Sequence
32	1131.4	92.9	7445	6	AR035974	AR035974 Sequence
33	1131.4	92.9	7445	6	AR035974	AR035974 Sequence
34	1131.4	92.9	7445	6	AR035974	AR035974 Sequence
35	1131.4	92.9	7729	6	AR035976	AR035976 Sequence
36	931.2	76.5	9472	6	AX287808	AX287808 Sequence
37	927.4	76.2	7599	12	SYNM13M9V	M77827 M13mp9 phag
38	927.4	76.2	7599	12	SYNM13M9V	M77827 M13mp9 phag
39	877	72.1	2000	6	SYNPUC9CPL	M77690 M13mp9/pUC9
40	835.6	68.7	151477	2	AC021926	I01987 Sequence 7
41	821.8	67.5	120538	2	AC015768	AC021926 Homo sapi
42	803.4	66.0	77945	2	AC022837	AC015768 Homo sapi
43	794.2	65.3	6407	7	INM13X	AC022837 Homo sapi
44	794.2	65.3	173561	2	AC016809	V00604 Phage M13 g
45	793.6	65.2	131156	2	AC015934	AC016809 Homo sapi

ALIGNMENTS

RESULT	1	AR036903	Sequence	1	from patent US 5800996.	1217 bp	DNA	linear	PAT 29-SEP-1999
LOCUS	AR036903	Sequence	1	from patent US 5800996.	1217 bp	DNA	linear	PAT 29-SEP-1999	
DEFINITION	AR036903	Sequence	1	from patent US 5800996.	1217 bp	DNA	linear	PAT 29-SEP-1999	
ACCESSION	AR036903	Sequence	1	from patent US 5800996.	1217 bp	DNA	linear	PAT 29-SEP-1999	
VERSION	AR036903.1	GI:5954759							
KEYWORDS									
SOURCE		Unknown.							
ORGANISM		Unknown.							
REFERENCE		1 (bases 1 to 1217)							
AUTHORS		Lee, L.G., Spurgeon, S.L. and Rosenblum, B.							
TITLE		Energy transfer dyes with enhanced fluorescence							
JOURNAL		Patent: US 5800996-A 1 01-SEP-1998;							
FEATURES		location/Qualifiers							
source		1. .1217							
BASE COUNT		335 a 291 c 321 g 270 t							
ORIGIN									

Query Match 100.0%; Score 1217; DB 6; Length 1217;
Best Local Similarity 100.0%; Pred. No. 0;

QY	1	GCCAAAGCTTGCAATGCCTGACAGTGCACACTAGAGGATCCCGGGTACCAGACTCGAATTTC	60
Db	1	GCCAAAGCTTGCAATGCCTGACAGTGCACACTAGAGGATCCCGGGTACCAGACTCGAATTTC	60
QY	61	GTAATCATGTGTCATAGCTGTTCTTCCTGTGTGAANTGTTATCCGTCACAATTCACACAA	120
Db	61	GTAATCATGTGTCATAGCTGTTCTTCCTGTGTGAANTGTTATCCGTCACAATTCACACAA	120
QY	121	CATPACGAGCGGAAGCATAAAGTGTAAAAGCCTGGGGTCCTTAATGAGTGAAGTCACTAC	180
Db	121	CATPACGAGCGGAAGCATAAAGTGTAAAAGCCTGGGGTCCTTAATGAGTGAAGTCACTAC	180
QY	181	ATTAATTTGGGTTGGCGTCACGTCCCGCTTCCAGTCGGGAAACCTGTCGCCAGCTGCA	240
Db	181	ATTAATTTGGGTTGGCGTCACGTCCCGCTTCCAGTCGGGAAACCTGTCGCCAGCTGCA	240
QY	241	TTAATGAATTCGGCCAACCGCGGGGAGAGGGGTTTCGGTATTGGGGCCAGGGTGGTTTT	300
Db	241	TTAATGAATTCGGCCAACCGCGGGGAGAGGGGTTTCGGTATTGGGGCCAGGGTGGTTTT	300
QY	301	TTCCTTTTACACAGTAGAGAGCGGCAACAGCTGATTGCCCTTCACCGCTTGCCTCTGAGAGA	360
Db	301	TTCCTTTTACACAGTAGAGAGCGGCAACAGCTGATTGCCCTTCACCGCTTGCCTCTGAGAGA	360
QY	361	GTTCGACGAAGCGGTGCACGCTGTTTTCGCCAGCAGCGGCGAATCCTGTTTGTATGGTGG	420
Db	361	GTTCGACGAAGCGGTGCACGCTGTTTTCGCCAGCAGCGGCGAATCCTGTTTGTATGGTGG	420
QY	421	TTCGGAATTCGGCAAAATTCCTTTATAATCAAAGAATAGCCCGAGATAGGCTTCAGTGT	480
Db	421	TTCGGAATTCGGCAAAATTCCTTTATAATCAAAGAATAGCCCGAGATAGGCTTCAGTGT	480
QY	481	TGTTCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGGACTCCAAGCTCAAAAGCGC	540
Db	481	TGTTCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGGACTCCAAGCTCAAAAGCGC	540
QY	541	AAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCAATCAAGTTTT	600
Db	541	AAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCAATCAAGTTTT	600
QY	601	GGGTCGAGTGCCTTAAGACCTAATCGGAACCTTAAGAGGAGCCCCGATTAGAGC	660
Db	601	GGGTCGAGTGCCTTAAGACCTAATCGGAACCTTAAGAGGAGCCCCGATTAGAGC	660
QY	661	TTGACGGGAAAGCCGGCAACGTGGCGAGAAGCAAGGAGAAAGCGGAAGAGCGGG	720
Db	661	TTGACGGGAAAGCCGGCAACGTGGCGAGAAGCAAGGAGAAAGCGGAAGAGCGGG	720
QY	721	CGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGGCGTACACCACACACCCGCGCGCT	780
Db	721	CGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGGCGTACACCACACACCCGCGCGCT	780
QY	781	TAATGCCCGCTACAGGGCGCTACTATGTTGCTTTGACGAGCACCTATAACGTGCTTT	840
Db	781	TAATGCCCGCTACAGGGCGCTACTATGTTGCTTTGACGAGCACCTATAACGTGCTTT	840
QY	841	CTCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCCGATTAAAGGATTTTACAGAGGA	900
Db	841	CTCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCCGATTAAAGGATTTTACAGAGGA	900
QY	901	ACGGTACGCGAATCTTGAGAGTGTTTTTATAATCAGTGAAGCCACCGAGTAAAGAG	960
Db	901	ACGGTACGCGAATCTTGAGAGTGTTTTTATAATCAGTGAAGCCACCGAGTAAAGAG	960
QY	961	TCCTGTCATCAGGCAATTAACCGTGTAGCAATCTCTTTGATTAGTAATAACATCAC	1020
Db	961	TCCTGTCATCAGGCAATTAACCGTGTAGCAATCTCTTTGATTAGTAATAACATCAC	1020
QY	1021	TTGCTGTAGTAGAAGAACTCAAACTATCGGCTTGCTGGTGAATATCCAGAACATATTAC	1080
Db	1021	TTGCTGTAGTAGAAGAACTCAAACTATCGGCTTGCTGGTGAATATCCAGAACATATTAC	1080


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Db 5329 TCTGTCCATCAGCAATTAACCGTTGTAGCAATACTTCTTGTATTAGTAATAACATCAC 5270
QY 1021 TTGCCTAGTAGAAGAACTCAAACTATCGGCCCTTGTGTGTAATATCCAGAACAAATATTAC 1080
Db 5269 TTGCCTAGTAGAAGAACTCAAACTATCGGCCCTTGTGTGTAATATCCAGAACAAATATTAC 5210
QY 1081 CGCAGCCATTCGACAGCAAAACGCTCATGGAATACCTACATTTGACGCTCAATCG 1140
Db 5209 CGCAGCCATTCGACAGCAAAACGCTCATGGAATACCTACATTTGACGCTCAATCG 5150
QY 1141 TCTGAATAGGATTTATACATTGGCAGATTACACGCTCAGCAGTCAACAGCAGTAAATAAGGGA 1200
Db 5149 TCTGAATAGGATTTATACATTGGCAGATTACACGCTCAGCAGTCAACAGCAGTAAATAAGGGA 5090
QY 1201 CATCTGGCCACAGAG 1217
Db 5089 CATCTGGCCACAGAG 5073

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RESULT 4
LOCUS SYNML3M18V/c 7250 bp DNA circular SYN 01-OCT-1993
DEFINITION M13mp18 phage cloning vector.
ACCESSION M77815
VERSION M77815.1 GI:208802
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE Obtained from VecBase 3.0
JOURNAL Unpublished (1991)
COMMENT These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Curator Program.

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TITLE M13mp18 - Phage cloning vector
DATE 03-FEB-1986
#sequence 02-APR-1986
ACCESSION V80018
SOURCE artificial
REFERENCE
#number 1
#authors Norrander J., Kempe T., Messing J.
#journal Gene (1983), 26: 101-106
#number 2
#authors Yanisch-Perron C., Vieira J., Messing J.
#journal Gene (1985) 33: 103-119
#comment shows the complete compiled sequence
REFERENCE
#number 3
#authors Dotto G.P., Zinder N.D.
#journal Nature (1984) 311: 279-280
#comment mutation: T at pos 6968, G at pos 6125 in M13 wildtype
REFERENCE
#number 4
#authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.
#book Cloning Vectors, Elsevier 1985 and supplements
#comment vector I-A-v-1
COMMENT
Obtained 3-MAR-1986 from J. Messing, Waksman Institute, NJ on floppy disc
Revised 02-APR-1986 by F. Pfeiffer, MPI, Martinsried
pos 898 TTT instead of TT to restore the gene v reading frame
KEYWORDS
CROSSREFERENCE
#prerevised
#parent
GenBank(50):M11454, EMBL(11):M13mp18
#parent
VecBase(3):M13mp10
#parent

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GenBank(50):M13, GenBank(50):EcoLac, VecSource(3):bGal18
#brother
VecBase(3):M13mp19
#offspring
VecBase(3):pUC18
PARENT
Features of M13mp18 (7250 bp)
residue source
1-5868 phage M13
5869-6230 936-1297 Lac-Operon
6231-6287 1- 57 M13mp18/pUC18-Polylinker
6290-6711 1303-1724 Lac-Operon
6712-7250 5869-6407 phage M13
Conflict (cfl) and Mutations (mut):
M13mp18 source
mut 3 T C 3 phage M13
mut 2220 A G 2220 phage M13
cfl 5977 G A 1044 Lac
cfl 6522 G T 1535 Lac
mut 6938 T C 6095 phage M13
mut 6968 T G 6125 phage M13
Position 898 is TT in Messing's sequence, but TTT in M13
wildtype.
it was changed to TTT to restore the reading frame of gene v.
M13mp18 does not contain amber mutations in gene I and gene II.
FEATURE
POLYLINKER EcoRI-SacI-KpnI-SmaI-BamHI-XbaI-SalI-PstI-SphI-HindIII
SELECTION
SUMMARY M13mp18 #length 7250 #checksum 7990.
#indicator beta-galactosidase
Location/Qualifiers
1..7250
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1768 a 1538 c 1533 g 2411 t
ORIGIN

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Query Match 99.9%; Score 1215.4; DB 12; Length 7250;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1216; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 GCCAAGCTGCATGCTGCAGGTGCGACTAGAGATCCCGGGTACCAGCTCGAATTC 60
Db 6290 GCCAAGCTGCATGCTGCAGGTGCGACTAGAGATCCCGGGTACCAGCTCGAATTC 6231
QY 61 GTAATCATGGTCATAGCTGTTTCTCTGTGTGAAATGTTATCCGCTCACAAATCCACAA 120
Db 6230 GTAATCATGGTCATAGCTGTTTCTCTGTGTGAAATGTTATCCGCTCACAAATCCACAA 6171
QY 121 CATACGACCGGAAAGCATAAAGTGTAAAGCCCTGGGTCCTAATGAGTGAGCTAACTAC 180
Db 6170 CATACGACCGGAAAGCATAAAGTGTAAAGCCCTGGGTCCTAATGAGTGAGCTAACTAC 6111
QY 181 ATTAATTCGTTGGCTCACTGCCGCTTCCAGTCGGGAAACCTGTCTGTCGACGTCGA 240
Db 6110 ATTAATTCGTTGGCTCACTGCCGCTTCCAGTCGGGAAACCTGTCTGTCGACGTCGA 6051
QY 241 TTAATGAATCGCCCAACGCGGGGAGAGGGGTTTGGCTATTGGCGCGCAGGGTGGTTT 300
Db 6050 TTAATGAATCGCCCAACGCGGGGAGAGGGGTTTGGCTATTGGCGCGCAGGGTGGTTT 5991
QY 301 TTCCTTTTACCAGTGAGACGGGCAACAGCTGATTCCTTCCCTTCCAGCTCGGCTGAGAGA 360
Db 5990 TTCCTTTTACCAGTGAGACGGGCAACAGCTGATTCCTTCCCTTCCAGCTCGGCTGAGAGA 5931
QY 361 GTTGACAGACGGCTCCACGCTGTTTGGCCCGCAGCGGAAATCCCTGTTGATGGTGG 420
Db 5930 GTTGACAGACGGCTCCACGCTGTTTGGCCCGCAGCGGAAATCCCTGTTGATGGTGG 5871
QY 421 TTCGGAATCGGCNAAATCCCTTATAAATCAAAAGATAGCCCCGAGATAGGGTTGAGTGT 480
Db 5870 TTCGGAATCGGCNAAATCCCTTATAAATCAAAAGATAGCCCCGAGATAGGGTTGAGTGT 5811

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Db 34223 TCCGGAATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGT 34164
Qy 481 TGTTCAGTTTGAACAAGAGTCCACTATTAAAGACGTTGGACTCCAAAGTCAAAAGGCG 540
Db 34163 TGTTCAGTTTGAACAAGAGTCCACTATTAAAGACGTTGGACTCCAAAGTCAAAAGGCG 34104
Qy 541 AAAACCGCTCTATCAGGCGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTT 600
Db 34103 AAAACCGCTCTATCAGGCGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTT 34044
Qy 601 GGGTCGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAGGAGCGCCCGATTTAGAGC 660
Db 34043 GGGTCGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAGGAGCGCCCGATTTAGAGC 33984
Qy 661 TTGACGGGAAAGCGCGGCAAGCTGGCGAGAAAGGAGGAAAGGAAAGGAGGAGCGG 720
Db 33983 TTGACGGGAAAGCGCGGCAAGCTGGCGAGAAAGGAGGAAAGGAGGAGGAGCGG 33924
Qy 721 CGTGTAGCGCGTGGCAAGTGTAGCGGTACGCTCGCGTAAACCAACACCGCGCGCT 780
Db 33923 CGTGTAGCGCGTGGCAAGTGTAGCGGTACGCTCGCGTAAACCAACACCGCGCGCT 33864
Qy 781 TAATGCGCGCTACAGGCGGTACTATGTTGCTTTGACGAGCAGCTATACCTGCTTT 840
Db 33863 TAATGCGCGCTACAGGCGGTACTATGTTGCTTTGACGAGCAGCTATACCTGCTTT 33804
Qy 841 CTTGCTTGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGGATTTAGACAGGA 900
Db 33803 CTTGCTTGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGGATTTAGACAGGA 33744
Qy 901 ACGGTACGCGAGAACTTGAAGAGTGTATTAATCAGTGAGCGCCACCGAGTAAAGAG 960
Db 33743 ACGGTACGCGAGAACTTGAAGAGTGTATTAATCAGTGAGCGCCACCGAGTAAAGAG 33684
Qy 961 TCTGTCCATCAGCAAAATTAACGTTGTAGCAATATCTTTGATTAAGTAAATCAATCAC 1020
Db 33683 TCTGTCCATCAGCAAAATTAACGTTGTAGCAATATCTTTGATTAAGTAAATCAATCAC 33624
Qy 1021 TTGCTGTAGTAGAAGCACTCAACATATCGGCTTGTGCTTAATATCCCAACAAATATAC 1080
Db 33623 TTGCTGTAGTAGAAGCACTCAACATATCGGCTTGTGCTTAATATCCCAACAAATATAC 33564
Qy 1081 GCCAGCATTTGCAACAGGAAAGGCTATGGAATACCTACATTTTACGCTCAATCG 1140
Db 33563 GCCAGCATTTGCAACAGGAAAGGCTATGGAATACCTACATTTTACGCTCAATCG 33504
Qy 1141 TCTCAATGGAATTTACATTTGCGAGATTACCA-GTCACAGCAGTAAATCAAGG 1199
Db 33503 TCTCAATGGAATTTACATTTGCGAGATTACCAATGTCACAGCAGTAAATCAAGG 33444
Qy 1200 ACATTCGCGCAACAGAG 1217
Db 33443 ATATTCGCGCAACAGAG 33426

RESULT 6
SYN13M10V/c
LOCUS SYN13M10V 7244 bp DNA circular SYN 26-JUL-1993
DEFINITION M13mp10 phage cloning vector.
ACCESSION L08819
VERSION L08819.1 GI:310747
KEYWORDS Synthetic construct DNA.
SOURCE ORGANISM
Synthetic construct
artificial sequence.
REFERENCE 1 (bases 1 to 7244)
AUTHORS Gilbert, W.
TITLE Obtained from VecBase 3.0
JOURNAL unpublished (1991)
COMMENT These data and their annotations were supplied to GenBank by Will Gilbert under the auspices of the GenBank Curator Program. M13mp10 - Phage cloning vector

ENTRY M13MP10
Phage cloning vector
DATE 27-MAR-1986
#sequence 02-APR-1986
ACCESSION V00016
SOURCE artificial
REFERENCE
#number 1
#authors Messing J., Vieira J.
#journal Gene (1982) 19: 269-276
#comment see note added in proof
REFERENCE
#number 2
#authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.
#book Cloning Vectors, Elsevier 1985 and supplements
#comment vector I-A-v-1
COMMENT
Assembled from M13mp18
by W. Gilbert, Whitaker College, MIT and
by F. Pfeiffer, MPI, Martinsried
KEYWORDS
CROSSREFERENCE
#parent
#parent VecBase(3):M13mp8
#brother
#brother VecBase(3):M13mp11
#offspring
#offspring VecBase(3):M13mp18, VecBase(3):M13mp17
PARENT
Features of M13mp10 (7244 bp)
residue source
1-5868 1-5868 phage M13
5869-6230 936-1297 Lac-Operon
6231-6281 1- 51 M13mp10/pUC12-Polylinker
6284-6705 1303-1724 Lac-Operon
6706-7244 5869-6407 phage M13
Conflict (cfl) and Mutations (mut):
M13mp10 source
mut 3 T C 3 phage M13
mut 2220 A G 2220 phage M13
cfl 5977 G A 1044 Lac
cfl 6516 G T 1535 Lac
mut 6932 T C 6095 phage M13
mut 6962 T G 6125 phage M13
Position 898 is TT in Messing's sequence, but TTT in M13
wildtype.
It was changed to TTT to restore the reading frame of gene V.
M13mp10a contains two amber mutations in gene I and gene II.
These mutations are not presented in this sequence.
In M13mp10w the mutations have been reverted to wildtype.
FEATURE
POLYLINKER EcoRI-SacI-SmaI-BamHI-XbaI-SalI-PstI-HindIII SELECTION
#indicator beta-galactosidase
SUMMARY M13mp10 #length 7244 #checksum 6839.
Location/Qualifiers
1..7244
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1766 a 1539 c 1530 g 2409 t
ORIGIN

Query Match 97.4%; Score 1184.8; DB 12; Length 7244;
Best Local Similarity 99.6%; Pred. No. 0;
Matches 1199; Conservative 0; Mismatches 2; Indels 3; Gaps 1;
Qy 14 GCCTGAGGTCGACTCTAGAGATCCCGGGTACCAGGCTCGAATTCGTAATCATGTGCA 73
Db 6274 GCCTGAGGTCGACTCTAGAGATCCCGGGTACCAGGCTCGAATTCGTAATCATGTGCA 6218
Qy 74 TAGCTGTTCTGCTGGAATTTGTTATCCGCTCACAATTCACACACATACGAGCGGGA 133

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Db	5137	ATTTCAGTTGGCAGATTACACAGTCAACAGCAGCAGTAAATAAAGGGACATTTCTGGCCCAAC	507
Qy	1214	AGAG 1217	
Db	5077	AGAG 5074	
RESULT	7		
LOCUS	108051/c	108051	9955 bp
DEFINITION	Sequence 7 from Patent EP 0265293.		
ACCESSION	108051		
VERSION	108051.1	GI:589240	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	1 (bases 1 to 9955)		
AUTHORS	Tabor, S. and Richardson, C.C.		
TITLE	T7 DNA polymerase		
JOURNAL	Patent: EP 0265293-A2 7 27-APR-1988;		
FEATURES	Location/Qualifiers		
source	1..9955		
BASE COUNT	2452 a 2218 c 2243 g 3039 t		
ORIGIN			
Query Match	95.7%;	Score 1165.2;	DB 6; Length 9955;
Best Local Similarity	99.7%;	Pred. No. 0;	
Matches 1167;	Conservative	0; Mismatches	3; Indels 0; Gaps
Qy	48	CGAGCTCGAATTCGTAAATCATGTGTCATAGCTGTTCCTGTGTGAAATTTGTTATCCGCTCA	107
Db	6243	CGAGCTCGAATTCGTAAATCATGTGTCATAGCTGTTCCTGTGTGAAATTTGTTATCCGCTCA	618
Qy	108	CAATTCACACAAACATACGAGCCGGGAAGCATAAAGTCTAAAGCTTGGGCTGCTTAATGAG	167
Db	6183	CAATTCACACAAACATACGAGCCGGGAAGCATAAAGTCTAAAGCTTGGGCTGCTTAATGAG	612
Qy	168	TGAGCTAACTCACATTAATTCGTTGGCTCACTGCCCGCTTTCCAGTCGGGAACCTGT	227
Db	6123	TGAGGTAACATCAATTAATTCGTTGGCTCACTGCCCGCTTTCCAGTCGGGAACCTGT	606
Qy	228	CGTCCAGCTGCATTAATGAATCGGCCAACCGCGGGGAGAGCGGTTTGGCTATTGGGC	28
Db	6063	CGTCCAGCTGCATTAATGAATTCGGCCAACCGCGGGGAGAGCGGTTTGGCTATTGGGC	606
Qy	288	GCCAGGCTGCTTTTCTTTTCCAGCAGTCAGACGGGCAACAGCTGATTCGCTTCCACGCG	34
Db	6003	GCCAGGCTGCTTTTCTTTTCCAGCAGTCAGACGGGCAACAGCTGATTCGCTTCCACGCG	59
Qy	348	TGGCCCTCAGAGAGTTGCAGCAAGCGGTCACGCTGCTTGGCCAGCAGCGGGAATCC	40
Db	5943	TGGCCCTCAGAGAGTTGCAGCAAGCGGTCACGCTGCTTGGCCAGCAGCGGGAATCC	58
Qy	408	TGTTTGATGCTGGTTCGCGAAATCGCAAAATCCCTTATATAATCAAAAGTAAGCCCGAGA	46
Db	5883	TGTTTGATGCTGGTTCGCGAAATCGCGAAATCCCTTATATAATCAAAAGTAAGCCCGAGA	58
Qy	468	TAGGTTTGAGTGTGTTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACCTGGACTCCA	52
Db	5823	TAGGTTTGAGTGTGTTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACCTGGACTCCA	57
Qy	528	ACGTCAAAAGGGCGAAACCGCTATACGGGGGATGGCCACTACCTACCTGAACCATCACCA	56
Db	5763	ACGTCAAAAGGGCGAAACCGCTATACGGGGGATGGCCACTACCTACCTGAACCATCACCA	5
Qy	588	AATCAAGTTTTTTTGGGTCGAGTGCCTGAAGCACTAAATTCGGAACCTTAAGGGAGCC	6
Db	5703	AATCAAGTTTTTTTGGGTCGAGTGCCTGAAGCACTAAATTCGGAACCTTAAGGGAGCC	5
Qy	648	CCCGATTAGAGCTTGACGGGGGAACGCCCGGACAGCTGGCGAGAAAGGAAGGAAGAAG	7

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Db 5643 CCCGATTAGAGCTTGACGGGAAAGCCGCGCAACCTGCGGAGAAAGGGAAGAAAG 5584
QY 708 CGAAGGAGCGGCGCTAGGCGCTGGCAAGCTTAGCGGTCACGCTGCGCGTAACACCA 767
Db 5583 CGAAGGAGCGGCGCTAGGCGCTGGCAAGCTTAGCGGTCACGCTGCGCGTAACACCA 5524
QY 768 CACCGCGCGGCTTAATGCGCGCTACAGGCGCGTACTATGTTGCTTTACAGACAG 827
Db 5523 CACCGCGCGGCTTAATGCGCGCTACAGGCGCGTACTATGTTGCTTTACAGACAG 5464
QY 828 TATAACCTGCTTTCCTGTTGGAATCAGAGCGGAGCTAAACAGAGCGCGGATTAAGGG 887
Db 5463 TATAACCTGCTTTCCTGTTGGAATCAGAGCGGAGCTAAACAGAGCGCGGATTAAGGG 5404
QY 888 ATTTTAGACAGGAGCTAGCGGCTAGCGGCTAGCGGCTAGCGGCTAGCGGCTAGCGG 947
Db 5403 ATTTTAGACAGGAGCTAGCGGCTAGCGGCTAGCGGCTAGCGGCTAGCGGCTAGCGG 5344
QY 948 CCGAGTAAAGAGCTGTCCTGTTGGAATCAGAGCGGAGCTAAACAGAGCGCGGATTAAGGG 1007
Db 5343 CCGAGTAAAGAGCTGTCCTGTTGGAATCAGAGCGGAGCTAAACAGAGCGCGGATTAAGGG 5284
QY 1008 GTAATACATCACTTCCCTGAGTAGAAGAACTCAAACTATCGGCTGCTGGTAATATCC 1067
Db 5283 GTAATACATCACTTCCCTGAGTAGAAGAACTCAAACTATCGGCTGCTGGTAATATCC 5224
QY 1068 AGACAATATTACCGCAGCCAGCTTGCACAGGAAACCTCATGGAATACCTACATTT 1127
Db 5223 AGACAATATTACCGCAGCCAGCTTGCACAGGAAACCTCATGGAATACCTACATTT 5164
QY 1128 TGACGCTCAATCTGCTGAATGGATTATTTACATGGCAGATTCACCGTACACAGCA 1187
Db 5163 TGACGCTCAATCTGCTGAATGGATTATTTACATGGCAGATTCACCGTACACAGCA 5104
QY 1188 GTAATAAAGGACATCTGCGCAACAGAG 1217
Db 5103 GTAATAAAGGACATCTGCGCAACAGAG 5074

RESULT 8
SYNMI3MP2V/c SYNMI3MP2V 7196 bp DNA circular SYN 26-JUL-1993
LOCUS MI3mp2 phase cloning vector.
DEFINITION L08818
ACCESSION L08818
VERSION L08818.1 GI:310751
KEYWORDS Synthetic construct DNA.
SOURCE artificial sequence.
ORGANISM Gilbert,W.
REFERENCE 1 (bases 1 to 7196)
AUTHORS Gilbert,W.
TITLE Obtained from VecBase 3.0
JOURNAL Unpublished (1991)
COMMENT These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program. MI3mp2
- Phase cloning vector
ENTRY MI3MP2 #TYPE DNA CIRCULAR TITLE MI3mp2 -
Phase cloning vector
DATE 27-MAR-1986
#sequence 02-APR-1986
ACCESSION V00012
SOURCE artificial
REFERENCE
#number 1
#authors Gronenborn B., Messing J.
#journal Nature (1978) 272: 375-377
COMMENT
Assembled from MI3mp7
by William Gilbert, Whitaker College, MIT and
by F. Pfeiffer, MPI, Martinsried
KEYWORDS
CROSSREFERENCE

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#parent
VecBase(3):MI3mp1
#parent
GenBank(50):M13, GenBank(50):EcoLac, GenBank(50):M13EcoLac
#offspring
VecBase(3):MI3mp7
PARENT
Features of MI3mp2 (7196 bp)
residue source
1-5868 1-5868 phase M13
5869-6230 936-1297 Lac-Operon
6231-6236 1-6 EcoRI site
6237-6657 1304-1724 Lac-Operon
6658-7196 5869-6407 phase M13
Conflict (cfl) and Mutations (mut):
MI3mp2 source
cfl 5977 G A 1044 Lac
cfl 6468 G T 1535 Lac
mut 6914 T G 6125 phase M13
Position 898 is TT in Messing's sequence, but TTT in M13
wildtype.
It was changed to TTT to restore the reading frame of gene v.
FEATURE
POLYLINKER none
SELECTION
#indicator beta-galactosidase
SUMMARY MI3mp2 #length 7196 #checksum 3751.
Location/Qualifiers
1..7196
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1757 a 1524 c 1516 g 2399 t
ORIGIN

Query Match 95.4%; Score 1161.4; DB 12; Length 7196;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 GAATTCGTAATCATGTGTCATAGCTGTTCTGTTGTAATTTGTTATCGCTCAAAATCC 114
Db 6236 GAATTCGTAATCATGTGTCATAGCTGTTCTGTTGTAATTTGTTATCGCTCAAAATCC 6177
QY 115 ACACAATACAGAGCGCGGAGCAATAAGTGTAAAGCTTGGGTGCCTAATGAGTGAGCTA 174
Db 6176 ACACAATACAGAGCGCGGAGCAATAAGTGTAAAGCTTGGGTGCCTAATGAGTGAGCTA 6117
QY 175 ACTCATTAAATGCGTTCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 234
Db 6116 ACTCATTAAATGCGTTCGCTCACTGCCGCTTTCCAGTCGGGAAACCTGTCGTGCCA 6057
QY 235 GCTGCATTAAATGAATCGGCAACGCGGAGAGCGGTTTGGCTATTTGGGCGCCAGG 294
Db 6056 GCTGCATTAAATGAATCGGCAACGCGGAGAGCGGTTTGGCTATTTGGGCGCCAGG 5997
QY 295 TGGTTTTCTTTTACCAGTGAGACGGGCAACAGCTGATTGCTTTCACCGCTGSCCCT 354
Db 5996 TGGTTTTCTTTTACCAGTGAGACGGGCAACAGCTGATTGCTTTCACCGCTGSCCCT 5937
QY 355 CAGAGAGTTGCAGCAAGCGTCCAGCTGTTGGCCAGCAGCGGAAAATCCTGTTTGA 414
Db 5936 CAGAGAGTTGCAGCAAGCGTCCAGCTGTTGGCCAGCAGCGGAAAATCCTGTTTGA 5877
QY 415 TGGTGGTTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGATACCCGAGATAGGTT 474
Db 5876 TGGTGGTTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGATACCCGAGATAGGTT 5817
QY 475 GAGTGGTTTCCAGCTTTGGAAACAGAGTCCACTATTAAGAACCTGGACTCCAACTCAA 534
Db 5816 GAGTGGTTTCCAGCTTTGGAAACAGAGTCCACTATTAAGAACCTGGACTCCAACTCAA 5757
QY 535 AGGCGGAAAAACCGCTTATCAGGCGGATGCCCACTACGTAACCATCACCAATCAAG 594

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QY 175 ACTCACAATTAATGGCTGGCTCACTGCCGCTTTCCAGTCGGGAACCTGCTGCCA 234
Db 6116 ACTCACAATTAATGGCTGGCTCACTGCCGCTTTCCAGTCGGGAACCTGCTGCCA 6057
QY 235 GCTGCATTAATGAATCGGCAACCGCGGAGAGGGGTTTCGTAATGGGCGCCAGGG 294
Db 6056 GCTGCATTAATGAATCGGCAACCGCGGAGAGGGGTTTCGTAATGGGCGCCAGGG 5997
QY 295 TGGTTTTTCTTTTCCACAGTGGAGCGGCAACAGCTGATTGGCCTTACCGCTGGCCCT 354
Db 5996 TGGTTTTTCTTTTCCACAGTGGAGCGGCAACAGCTGATTGGCCTTACCGCTGGCCCT 5937
QY 355 GAGAGAGTTGACAGAGCGCTCCAGCTGGTTGGCCCGAGCGGAAATCTGTTTCA 414
Db 5936 GAGAGAGTTGACAGAGCGCTCCAGCTGGTTGGCCCGAGCGGAAATCTGTTTCA 5877
QY 415 TGGTGGTTCCGAAATCGGCAAAATCCCTTATAAATCAAAGAAATAGCCGAGATAGGTT 474
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Db 5816 GAGTGTGTTCCAGTTTGGACAGAGTCCACTATTAAAGAACCTGGACTCAACCTCAA 5757
QY 535 AGGCGGAAACACCTCTATCAGGCGGATGGCCCACTAGTGAACCATCACCAATCAAG 594
Db 5756 AGGCGGAAACACCTCTATCAGGCGGATGGCCCACTAGTGAACCATCACCAATCAAG 5697
QY 595 TTTTGGGTCGAGGTGCGCTTAAGCACTAAATCGGAACCTTAAGGGAGCCCGCGATT 654
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QY 655 TAGAGCTTGACGGGGAAGCGCGAACGTGGGAGAAAGAGGAGGAAAGCAAGG 714
Db 5636 TAGAGCTTGACGGGGAAGCGCGAACGTGGGAGAAAGAGGAGGAAAGCAAGG 5577
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QY 775 CCGGCTTAATGCGCGCTACAGGGCGCTACTATGCTTGTGACGACGACGATTAAG 834
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Db 5456 TGTCTTCTCTGTTGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGGATTTAG 5397
QY 895 ACAGGACGGTACGCCAGATCTTGAGAGTGTGTTTATAATCAGTGAGGCCACCGAGTA 954
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Db 5336 AAAGAGTGTCTCCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTAATA 5277
QY 1015 CATCACTTGGCTGAGTGAAGAACTCAAACTATCGGCTTCTGTAATATCCAGAACAA 1074
Db 5276 CATCACTTGGCTGAGTGAAGAACTCAAACTATCGGCTTCTGTAATATCCAGAACAA 5217
QY 1075 TATTACCGCCAGCATTTGCAACAGGAAACGCTCATGGAATACCTACATTTTACGCT 1134
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QY 1135 CAATCTGCTGAATGATTATTTACATTTGGCAGATTCACCAAGTACACAGCAGTAATA 1194
Db 5156 CAATCTGCTGAATGATTATTTACATTTGGCAGATTCACCAAGTACACAGCAGTAATA 5097
QY 1195 AAGGGACATTTCTGGCCCAACAGAG 1217
Db 5096 AAGGGACATTTCTGGCCCAACAGAG 5074
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RESULT 10
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LOCUS SYNPUC8CPL 7229 bp ss-DNA linear SYN 07-MAR-2000
DEFINITION M13mp8/pUC8 cloning vector.
ACCESSION M77689
VERSION 1
KEYWORDS beta-galactosidase; lac gene.
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (sites)
AUTHORS Vieira, J. and Messing, J.
TITLE The pUC plasmids, an M13mp7-derived system for insertion
JOURNAL mutagenesis and sequencing with synthetic universal primers
MEDLINE Gene 19, 259-268 (1982)
REFERENCE 2 (bases 1 to 7229)
AUTHORS Messing, J. and Vieira, J.
TITLE A new pair of M13 vectors for selecting either DNA strand of
JOURNAL double-digest restriction fragments
MEDLINE Gene 19, 269-276 (1982)
FEATURES
source Location/Qualifiers
1..7229
/organism="synthetic construct"
/db_xref="taxon:32630"
/focus
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/organism="Coliphage M13"
/db_xref="taxon:10870"
5869..6230
/organism="Escherichia coli"
/notes="Lac-Operon"
/db_xref="taxon:562"
6231..6266
/organism="synthetic construct"
/notes="M13mp8/pUC8-Polylinker"
/db_xref="taxon:32630"
6269..6690
/organism="Escherichia coli"
/db_xref="taxon:562"
6691..7229
/organism="Coliphage M13"
/db_xref="taxon:10870"
BASE COUNT 1763 a 1534 c 1526 g 2406 t
ORIGIN
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Query Match 95.4%; Score 1161.4; DB 12; Length 7229;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 55 GAATTCGTAATCATGTCATAGCTGTTCTCTGTGTAATAATGTTATCCGCTCACAATTC 114
Db 6236 GAATTCGTAATCATGTCATAGCTGTTCTCTGTGTAATAATGTTATCCGCTCACAATTC 6177
QY 115 ACACAACATACAGCGCGGAAAGCATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGTA 174
Db 6176 ACACAACATACAGCGCGGAAAGCATAAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGTA 6117
QY 175 ACTCATTAAATGCTGCTCACTGCCGCTTTCAGTCGGGAAACCTGTGCTGCCA 234
Db 6116 ACTCATTAAATGCTGCTCACTGCCGCTTTCAGTCGGGAAACCTGTGCTGCCA 6057
QY 235 GCTGCATTAATGAATCGGCAACCGCGGAGAGGGGTTTCGTAATGGGCGCCAGGG 294
Db 6056 GCTGCATTAATGAATCGGCAACCGCGGAGAGGGGTTTCGTAATGGGCGCCAGGG 5997
QY 295 TGGTTTTTCTTTTCCACAGTGGAGCGGCAACAGCTGATTGGCCTTACCGCTGGCCCT 354
Db 5996 TGGTTTTTCTTTTCCACAGTGGAGCGGCAACAGCTGATTGGCCTTACCGCTGGCCCT 5937
QY 355 GAGAGAGTTGACAGGAGCGGTCCAGCTGTTTGGCCCGAGCGGAAATCTGTTTGA 414
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Db 5936 GAGAGAGTTGCACGAAGCGTCCACGCTGTTGCCCCAGCGGCAAAATCCTGTTGA 5877
QY 415 TGCTGTTCCGAATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGTT 474
Db 5876 TGCTGTTCCGAATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGTT 5817
QY 475 GAGTGTGTTCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTTGGACTCCACGTTCAA 534
Db 5816 GAGTGTGTTCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTTGGACTCCACGTTCAA 5757
QY 535 AGGCGCAAAACCGCTTCTACAGGCGGATGCCCACTAGCTGAACCATCACCAATCAAG 594
Db 5756 AGGCGCAAAACCGCTTCTACAGGCGGATGCCCACTAGCTGAACCATCACCAATCAAG 5697
QY 595 TTTTGGGGTTCGAGTGGCCGCTAAAGCACTAAATCGGAACCTTAAGGGAGCCCGCCGATT 654
Db 5696 TTTTGGGGTTCGAGTGGCCGCTAAAGCACTAAATCGGAACCTTAAGGGAGCCCGCCGATT 5637
QY 655 TAGAGCTTTAGCGGGGAAAGCGCGCAACGTTGGCGAGAAAGGGAAGGAAAGCGAAAG 714
Db 5636 TAGAGCTTTAGCGGGGAAAGCGCGCAACGTTGGCGAGAAAGGGAAGGAAAGCGAAAG 5577
QY 715 AGCGGCGCTAGGCGCTGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACACCGCG 774
Db 5576 AGCGGCGCTAGGCGCTGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACACCGCG 5517
QY 775 CGCGCTTAATGCGCGCTACAGGCGGCTACTATGTTGTTGACGACGACGTAACG 834
Db 5516 CGCGCTTAATGCGCGCTACAGGCGGCTACTATGTTGTTGACGACGACGTAACG 894
QY 835 TGCTTTCTCTGTTGGAATCAGAGCGGAGCTAAACAGAGGCGGATTAAGGGATTTTAG 5397
Db 5456 TGCTTTCTCTGTTGGAATCAGAGCGGAGCTAAACAGAGGCGGATTAAGGGATTTTAG 5397
QY 895 ACAGGAACGTTAGCGCAGAAATCTCAGAGTGTGTTTATATCACTGAGGCGCACGAGTA 954
Db 5396 ACAGGAACGTTAGCGCAGAAATCTCAGAGTGTGTTTATATCACTGAGGCGCACGAGTA 5337
QY 955 AAAGAGTCTGTCATCAGCAAAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAATA 1014
Db 5336 AAAGAGTCTGTCATCAGCAAAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAATA 5277
QY 1015 CATCACTTGCCTGAGTAGAAGAACTCAAACTATCGGCTTCTGCTGGTAAATATCCAGAACAA 1074
Db 5276 CATCACTTGCCTGAGTAGAAGAACTCAAACTATCGGCTTCTGCTGGTAAATATCCAGAACAA 5217
QY 1075 TATTACCGCCAGCCATTGCCACAGGAAACCGCTCATGGAATACCTTACATTTTGAGCT 1134
Db 5216 TATTACCGCCAGCCATTGCCACAGGAAACCGCTCATGGAATACCTTACATTTTGAGCT 5157
QY 1135 CAATGCTCTGAAATGGATTATTTACATTGGCAGATTCCACGTCACACGACGAGTAATA 1194
Db 5156 CAATGCTCTGAAATGGATTATTTACATTGGCAGATTCCACGTCACACGACGAGTAATA 5097
QY 1195 AAGGGACATTTCTGCCACACAGAG 1217
Db 5096 AAGGGACATTTCTGCCACACAGAG 5074

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RESULT 12
LOCUS SYN13MP7V/c 7238 bp DNA circular SYN 27-APR-1993
DEFINITION M13mp7 phage cloning vector.
ACCESSION M77669 M25456
VERSION M77669.1 GI:208803
KEYWORDS
SOURCE Synthetic construct DNA.
ORGANISM synthetic construct
REFERENCE 1 (sites)
AUTHORS Messing, J., Crea, R., and Seeburg, P.H.
TITLE A system for shotgun DNA sequencing
JOURNAL Nucleic Acids Res. 9, 309-321 (1981)

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81150468
2 (sites)
Vieira, J. and Messing, J.
The pUC plasmids, an M13mp7-derived system for insertion
mutagenesis and sequencing with synthetic universal primers
Gene 19, 259-268 (1984)
83106470
3 (bases 1 to 7238)
Gilbert, W.
Obtained from VecBase 3.0
Unpublished (1991)
These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program. M13mp7
ENTRY M13MP7
Phage cloning vector
#TYPE DNA CIRCULAR TITLE M13mp7 -
DATE 27-MAR-1986
#sequence 02-APR-1986
ACCESSION VB0013
SOURCE artificial
REFERENCE
#number 1
#authors Messing J., Crea R., Seeburg P.H.
#journal Nucleic Acids Res. (1981) 9: 309-321
#title A system for shotgun DNA sequencing
REFERENCE
#number 2
#authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.
#book Cloning Vectors, Elsevier 1985 and supplements
#comment vector I-A-V-1
COMMENT
Assembled from M13mp8
by William Gilbert, Whitaker College, MIT and
by F. Pfeiffer, MPI, Martinsried
KEYWORDS
CROSSREFERENCE
#parent
VecBase(3):M13mp2
#parent
GenBank(50):M13, GenBank(50):EcoLac, VecSource(3):bgal7
#offspring
VecBase(3):pUC7, VecBase(3):M13mp8, VecBase(3):M13mp9
VecBase(3):M13tg130, VecBase(3):M13tg131
PARENT
Features of M13mp7 (7238 bp)
residue source
1-5868 1-5868 phage M13
5869-6230 936-1297 Lac-Operon
6231-6278 1- 48 M13mp7/pUC7-PolyLinker
6279-6699 1304-1724 Lac-Operon
6700-7238 5869-6407 phage M13
Conflict (cfl) and Mutations (mut):
M13mp7 source
mut 3 T C 3 phage M13
mut 2220 A G 2220 phage M13
cfl 5977 G A 1044 Lac
cfl 6510 G T 1535 Lac
mut 6926 T C 6095 phage M13
mut 6956 T G 6125 phage M13
#comment
Position 898 is TT in Messing's sequence, but TTT in M13
wildtype.
It was changed to TTT to restore the reading frame of gene V.
#comment
M13mp7 contains two amber mutations in M13 gene I and gene II.
These mutations are not presented in this sequence. FEATURE
POLYLINKER EcoRI-BamHI-SalI-PstI-SalI-BamHI-EcoRI SELECTION
#indicator beta-galactosidase
SUMMARY M13mp7 #length 7238 #checksum 8176.
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"

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FEATURES
source

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Best Local Similarity	99.9%; Pred. No. 0;				
Matches 1162; Conservative	0; Mismatches 1; Indels 0; Gaps 0;				
QY	55 GAATTCGTAATCATGTCATAGCTGTTTCCGTGTGCAAAATGTTATCCGCTCAACAATCC 114				
Db	6236 GAATTCGTAATCATGTCATAGCTGTTTCCGTGTGCAAAATGTTATCCGCTCAACAATCC 6177				
QY	115 ACACAAATACAGCGCGGAGGATAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 174				
Db	6176 ACACAAATACAGCGCGGAGGATAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTA 6117				
QY	175 ACTCAGATTAATGTCGTCCTGCTCAGTCCCGCTTTCCAGTCGGGAACCTGTCGTGCCA 234				
Db	6116 ACTCAGATTAATGTCGTCCTGCTCAGTCCCGCTTTCCAGTCGGGAACCTGTCGTGCCA 6057				
QY	235 GCTGCATTAATGAATCGGCAACCGCGGAGAGGCGGTTTGCCTATTGGGGCCAGGG 294				
Db	6056 GCTGCATTAATGAATCGGCAACCGCGGAGAGGCGGTTTGCCTATTGGGGCCAGGG 5997				
QY	295 TGGTTTCTTTTTCACAGTGAGAGCGGCAACAGCTGATTCGCCCTTCCCGCCCTGGCCCT 354				
Db	5996 TGGTTTCTTTTTCACAGTGAGAGCGGCAACAGCTGATTCGCCCTTCCCGCCCTGGCCCT 5937				
QY	355 GAGAGAGTTCAGCAAGCGTCCACGCTGTTTCCCGCAGCGAGCGAAATTCCTGTTGA 414				
Db	5936 GAGAGAGTTCAGCAAGCGTCCACGCTGTTTCCCGCAGCGAGCGAAATTCCTGTTGA 5877				
QY	415 TGGTGTTCGCAATCGGCAAAATCCCTTATAATCAAAAGAAATAGCCCGAGATAGGTT 474				
Db	5876 TGGTGTTCGCAATCGGCAAAATCCCTTATAATCAAAAGAAATAGCCCGAGATAGGTT 5817				
QY	475 GAGTGTTCGCAATCGGCAAAATCCCTTATAATCAAAAGAAATAGCCCGAGATAGGTT 534				
Db	5816 GAGTGTTCGCAATCGGCAAAATCCCTTATAATCAAAAGAAATAGCCCGAGATAGGTT 5757				
QY	535 AGGCGGAAATACCGTCTATCAGGCGGATGCGCCACTAGCTGAACCATCACCCAAATCAAG 594				
Db	5756 AGGCGGAAATACCGTCTATCAGGCGGATGCGCCACTAGCTGAACCATCACCCAAATCAAG 5697				
QY	595 TTTTTCGGGTCGAGGTCGCTTAAAGCACTAAATCGGAAACCTTAAGGAGGCCCCCGATT 654				
Db	5696 TTTTTCGGGTCGAGGTCGCTTAAAGCACTAAATCGGAAACCTTAAGGAGGCCCCCGATT 5637				
QY	655 TAGAGCTTGCGGGAAGCGCGCAACGCTGGCGAGAAAGGAAAGGAAAGCGAAAGG 714				
Db	5636 TAGAGCTTGCGGGAAGCGCGCAACGCTGGCGAGAAAGGAAAGGAAAGCGAAAGG 5577				
QY	715 AGCGGCGCTAGGCGCTGGCAAGTGTAGCGGTACGCTGCGGCTGAACCAACACACCCCG 774				
Db	5576 AGCGGCGCTAGGCGCTGGCAAGTGTAGCGGTACGCTGCGGCTGAACCAACACACCCCG 5517				
QY	775 CGCGCTTAATGCGCGCTACAGGCGCGCTACTATGTTGCTTTCAGGAGCAGCTATAAG 834				
Db	5516 CGCGCTTAATGCGCGCTACAGGCGCGCTACTATGTTGCTTTCAGGAGCAGCTATAAG 5457				
QY	835 TGCTTTCCTGCTTGGAAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGAGGATTTAG 894				
Db	5456 TGCTTTCCTGCTTGGAAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGAGGATTTAG 5397				
QY	895 ACAGGAACGGTACGCGAGAAATCTTGAGAGTGTGTTTATATCATCAGTGAGGCGCCAGGTA 954				
Db	5396 ACAGGAACGGTACGCGAGAAATCTTGAGAGTGTGTTTATATCATCAGTGAGGCGCCAGGTA 5337				
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QY 1075 TATTACCGCCAGCCATTGCAACAGGAAAGCGCTCATGGAATACCTTACATTTTGACGCT 1134

Db 5216 TATTACCGCCAGCCATTGCAACAGGAAAGCGCTCATGGAATACCTTACATTTTGACGCT 5157

QY 1135 CAATCGTCTGAAATGGGATTTTACATTTGGCAGATTACACAGTCCACAGCAGCAGTAATAA 1194

Db 5156 CAATCGTCTGAAATGGGATTTTACATTTGGCAGATTACACAGTCCACAGCAGCAGTAATAA 5097

QY 1195 AAGGACATTTCTGGCCCAACAGAG 1217

Db 5096 AAGGACATTTCTGGCCCAACAGAG 5074

RESULT 13

SYNTG130V/c

LOCUS SYNTG130V 7265 bp DNA circular SYN 26-JUL-1993

DEFINITION M13tg130 phage cloning vector.

ACCESSION L08828

VERSION L08828.1 GI:310852

KEYWORDS Synthetic construct DNA.

SOURCE synthetic construct

ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 7265)

AUTHORS Gilbert,W

TITLE Obtained from VecBase 3.0

JOURNAL Unpublished (1991)

COMMENT These data and their annotation were supplied to GenBank by Will Gilbert under the auspices of the GenBank Curator Program.

M13tg130 - Phage Cloning Vector

ENTRY M13tg130 #TYPE DNA CIRCULAR TITLE M13tg130

DATE 19-DEC-1986

ACCESSION VB0054

SOURCE artificial

REFERENCE

#number 1

#authors Kieny M.P., Lathe R., Lecocq J.P.

#journal Gene (1983) 26: 91-99

REFERENCE

#number 2

#authors Pouwels P.H., Enger-Valk B.E., Brammar W.J.

#book Cloning Vectors, Elsevier 1985 and supplements

#comment vector I-A-v-1

COMMENT Assembled from M13mp7 and M13tg130-Polylinker by F. Pfeiffer

KEYWORDS

CROSSREFERENCE

#parent VecBase(3):M13mp7, GenBank(50):M13tg130,

VecSource(3):bGal130

#brother VecBase(3):M13tg131

#offspring VecBase(3):pUC830, VecBase(3):pOM2, VecBase(3):pOM4,

VecBase(3):pOM8

PARENT

Features of M13tg130 (7265 bp)

residue source

1-6230 1-6230 M13mp7

6231-6299 1- 69 M13tg130-Polylinker

6300-7265 6273-7238 M13mp7

Conflict (cfl) and Mutations (mut): none

FEATURE

POLYLINKER

ECORI-SmaI-EcoRV-SphI-KpnI-XbaI-HindIII-BamHI-SalI-PstI

SELECTION

#indicator beta-galactosidase

SUMMARY M13tg130 #length 7265 #checksum 2344.

Location/Qualifiers

FEATURES

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/organism="synthetic construct"
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Query Match 95.4%; Score 1161.4; DB 12; Length 7265;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1162; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 55 GAATTCGTAATCATAGTGCATAGCTGTTTCTCTGTGTGAATTTGTTATCCCGTCACAATTC 114
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QY 115 ACACACATACAGCGCGGAGCAATAAGTGTAAAGCTGGGCTGCCTAATGAGTGAGCTA 174
Db 6176 ACACACATACAGCGCGGAGCAATAAGTGTAAAGCTGGGCTGCCTAATGAGTGAGCTA 6117

QY 175 ACTCACAATTAATTCGGTTCGGTCACTGCGCGTTTCCAGTCGGGAAACCTGTCGTGCCA 234
Db 6116 ACTCACAATTAATTCGGTTCGGTCACTGCGCGTTTCCAGTCGGGAAACCTGTCGTGCCA 6057

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Db 6056 GCTGCATTAATGAATCGGCAACCGCGGAGAGCGGTTTTCGATTTGGGCGCCAGG 5997

QY 295 TGGTTTTCCTTTCACAGTACAGCGGCAACAGCTGATTTGCCCTTTCACGCGCTGGCCCT 354
Db 5996 TGGTTTTCCTTTCACAGTACAGCGGCAACAGCTGATTTGCCCTTTCACGCGCTGGCCCT 5937

QY 355 GAGAGAGTTGACGAGCGGTCACGCTGTTTTCGCGGAGAGCGGCAACAGCTGATTTGCCCTTTCACGCGCTGGCCCT 414
Db 5936 GAGAGAGTTGACGAGCGGTCACGCTGTTTTCGCGGAGAGCGGCAACAGCTGATTTGCCCTTTCACGCGCTGGCCCT 5877

QY 415 TGGTGTTCGGAATTCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGGTT 474
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Db 5816 GAGTGTTCGTCAGTTTGGCAACAGAGTCCACTAATTAAGAACGTTGGACTCCAGCTCAA 5757

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QY 595 TTTTTCGGGTTCGAGGTCCGCTAAGCACTAAATCGGAACCTTAAGAGGAGCCCGGAT 654
Db 5696 TTTTTCGGGTTCGAGGTCCGCTAAGCACTAAATCGGAACCTTAAGAGGAGCCCGGAT 5637

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Db 5636 TAGAGCTTGACGGGAAAGCGCGGAACGTTGGCGAGAAAGGAGGAGAAAGGAAAGG 5577

QY 715 AGCGGGCGCTAGGCGGTGCAAGTGTAGCGGTACCGTCCGCTAACCCACACCCCGC 774
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QY 775 CGCGCTTAATTCGCGCGTACAGGCGGCTACTATGTTGCTTTCACGAGCACGTATAAG 834
Db 5516 CGCGCTTAATTCGCGCGTACAGGCGGCTACTATGTTGCTTTCACGAGCACGTATAAG 5457

QY 835 TGCTTTCCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTTAAAGGATTTTAG 894
Db 5456 TGCTTTCCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTTAAAGGATTTTAG 5397

QY 895 ACAGGAACGCTACCGCAGAACTCTTGAAGTGTGTTTATAATCAGTGAGGCCACCGAGTA 954
Db 5396 ACAGGAACGCTACCGCAGAACTCTTGAAGTGTGTTTATAATCAGTGAGGCCACCGAGTA 5337

QY 955 AAAGAGTCTGTCCATCACGCAAAATTAACCGTTGTAGCAATACATCTTCTTATTAGTAATA 1014
Db 955 AAAGAGTCTGTCCATCACGCAAAATTAACCGTTGTAGCAATACATCTTCTTATTAGTAATA 1014

Db 5336 AAAGAGTCTGTCCATCACGCAAAATTAACCGTTGTAGCAATACATCTTCTTATTAGTAATA 5277
QY 1015 CATCACTTGCCTGAGTAGAAGAACTCAAACTATCGCGCTTGCCTGTAATATCCAGAACAA 1074
Db 5276 CATCACTTGCCTGAGTAGAAGAACTCAAACTATCGCGCTTGCCTGTAATATCCAGAACAA 5217
QY 1075 TATTACCGCCAGCCATTGCAACAGAGAAACGCTCATGGAATACCTACATTTTGACGCT 1134
Db 5216 TATTACCGCCAGCCATTGCAACAGAGAAACGCTCATGGAATACCTACATTTTGACGCT 5157
QY 1135 CAATCGTCTGAAATGGATTTATTACATTTGGCAGATTCCACGAGTACAGCAGCAAGTAATA 1194
Db 5156 CAATCGTCTGAAATGGATTTATTACATTTGGCAGATTCCACGAGTACAGCAGCAAGTAATA 5097
QY 1195 AAGGACATTTCTGCCCAACAGAG 1217
Db 5096 AAGGACATTTCTGCCCAACAGAG 5074

RESULT 14
SYNM13MP1V/c SYNM13MP1V 7196 bp DNA circular SYN 26-JUL-1993
LOCUS M13mpl1 phage cloning vector.
DEFINITION L08813
ACCESSION L08813.1 GI:310750
VERSION L08813.1
KEYWORDS Synthetic construct DNA.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 7196)
AUTHORS Gilbert,W.
TITLE Obtained from VecBase 3.0
JOURNAL Unpublished (1991)
COMMENT These data and their annotation were supplied to GenBank by Will
Gilbert under the auspices of the GenBank Curator Program. M13mpl1
- Phage cloning vector
ENTRY M13MP1
Phage cloning vector
DATE 27-MAR-1986
#sequence 02-APR-1986
ACCESSION V00011
SOURCE artificial
REFERENCE
#number 1
#journal Messing J., Gronenborn B., Mueller-Hill B.,
Hofschneider P.H.
Proc. Nat. Acad. Sci. USA (1977) 74: 3642-3646
#number 2
#authors Dotto G.P., Zinder N.D.
#journal Nature (1984) 311: 279-280
#comment mutation: T at pos 6914, G at pos 6125 in M13 wildtype
COMMENT
Assembled from M13mp2
by William Gilbert, Whitaker College, MIT and
by F. Pfeiffer, MPI, Martinsried
KEYWORDS
CROSSREFERENCE
#parent
GenBank(50):M13, GenBank(50):EcoLac
#offspring
VecBase(3):M13mp2
PARENT
Features of M13mpl1 (7196 bp)
residue source
1-5868 1-5868 phage M13
5869-6657 936-1724 Lac-Operon
6658-7196 5869-6407 phage M13
Conflict (cfl) and Mutations (mut):
M13mpl1 source
cfl 5977 G A 1044 Lac
cfl 6468 G T 1535 Lac
mut 6914 T G 6125 phage M13
```


Features of M13tg131 (7265 bp)
residue source
1-6232 M13mp7
6233-6305 1- 73 M13tg131-Polylinker
6306-7265 6279-7238 M13mp7
Conflict (cfl) and Mutations (mut): none
FEATURE
POLYLINKER (BglII)-PstI-SalI-BamHI-HindIII-XbaI-
KpnI-SphI-EcoRV-SstI-SmaI-EcoRI
SELECTION
#indicator beta-galactosidase
SUMMARY M13tg131 #length 7265 #checksum 2704.
Location/Qualifiers
1. 7265
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 1772 a 1543 c 1534 g 2416 t
ORIGIN

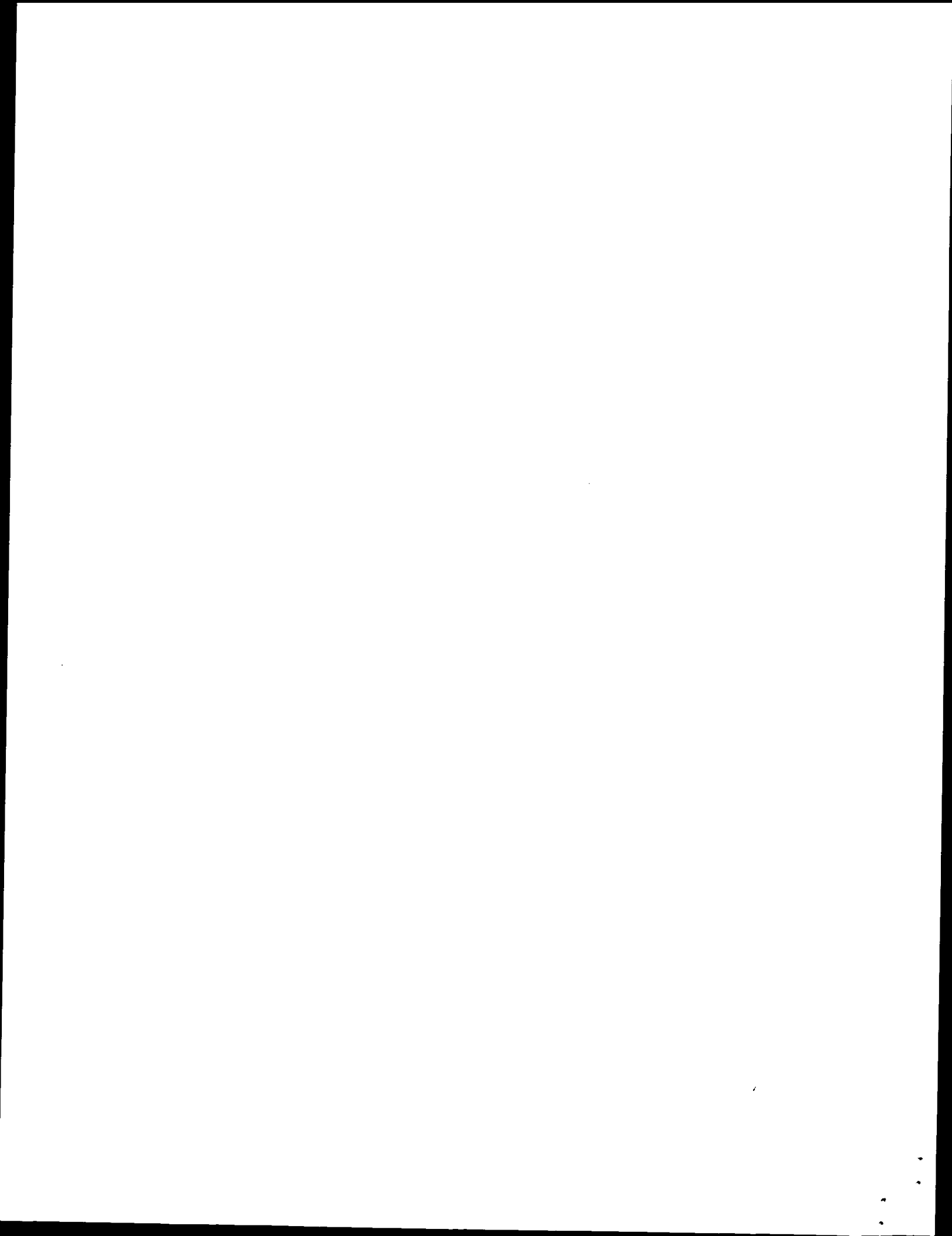
Query Match 95.1%; Score 1156.8; DB 12; Length 7265;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1158; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 58 TTGCTAATCATGTCTAGTGTTCCTGTGTGAATTTGTTATCCGCTCAAAATTCACAA 117
DB 6233 TGGCTAATCATGTCTAGTGTTCCTGTGTGAATTTGTTATCCGCTCAAAATTCACAA 6174
QY 118 CAACATACAGCGCGGAGCAATTAAGTGAAGCCTGGGTGCTTAATAGTGAGCTAACT 177
DB 6173 CAACATACAGCGCGGAGCAATTAAGTGAAGCCTGGGTGCTTAATAGTGAGCTAACT 6114
QY 178 CACATTAATTTGGCTTGGCTCTACTGCGCCCTTCCAGCTCGGGAACCTGTCTGCCAGCT 237
DB 6113 CACATTAATTTGGCTTGGCTCTACTGCGCCCTTCCAGCTCGGGAACCTGTCTGCCAGCT 6054
QY 238 GCATTAATGAATCGGCCCAACGGCGGGAGAGCGGTTCGCTATTGGCGCCACGGGTGG 297
DB 6053 GCATTAATGAATCGGCCCAACGGCGGGAGAGCGGTTCGCTATTGGCGCCACGGGTGG 5994
QY 298 TTTTCTTTTCCAGCTGAGAGCGGCAACAGCTGATTCGCCCTTCACCGCTGGCCCTGAG 357
DB 5993 TTTTCTTTTCCAGCTGAGAGCGGCAACAGCTGATTCGCCCTTCACCGCTGGCCCTGAG 5934
QY 358 AGAGTTCGAGCAAGGGTCCAGCTGTTTCCCGCAGCGGCAAAATCCCTGTTTGATGG 417
DB 5933 AGAGTTCGAGCAAGGGTCCAGCTGTTTCCCGCAGCGGCAAAATCCCTGTTTGATGG 5874
QY 418 TGGTTCGGAATCGCAAAATCCCTTATAATCAAAAGATAGCCCGAGATAGGTTGAG 477
DB 5873 TGGTTCGGAATCGCAAAATCCCTTATAATCAAAAGATAGCCCGAGATAGGTTGAG 5814
QY 478 TGTGTTCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGGACTCCCAACGTCAAAGG 537
DB 5813 TGTGTTCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGGACTCCCAACGTCAAAGG 5754
QY 538 GCGAAAAACCGTCTATCAGGCGCATGCCCTACCTGTAACCTATCAACCAATCAAGTTT 597
DB 5753 GCGAAAAACCGTCTATCAGGCGCATGCCCTACCTGTAACCTATCAACCAATCAAGTTT 5694
QY 598 TTTGGGGTCCAGGTGCGGTAAAGCACTATAATCGGAACCTTAAAGGGAGCCCGGATTTAG 657
DB 5693 TTTGGGGTCCAGGTGCGGTAAAGCACTATAATCGGAACCTTAAAGGGAGCCCGGATTTAG 5634
QY 658 AGCTTCAGCGGGAACCGCGCAACGTGGCGGAAAGGAAGGAAGGAAGGAAGGAGG 717
DB 5633 AGCTTCAGCGGGAACCGCGCAACGTGGCGGAAAGGAAGGAAGGAAGGAAGGAGG 5574
QY 718 GGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCGCCCG 777
DB 5573 GGGCGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCGCCCG 5514
QY 778 GCTTAATGCGCCCTACAGGCGCGGTACTATGTTGCTTTGACGAGCAGGTAAACGTGC 837

Search completed: August 1, 2002, 09:29:47
Job time: 6593 sec

us-10-014-743-1.rge

Thu Aug 1 12:08:38 2002



Thu Aug 1 12:08:39 2002

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 07:44:44 ; Search time 365.16 seconds

(without alignments)
5722.108 Million cell updates/sec

Title: US-10-014-743-1

Perfect score: 1217

Sequence: 1 GCCAAGCTTGCATGCTGCA.....GGACATTCGTGCCAACAGAG 1217

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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- 2: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
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- 4: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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- 22: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1217	100.0	1217	18 AAV12871	M13 DNA sequence.
2	1217	100.0	1217	20 AAZ09714	Bacteriophage M13
3	1217	100.0	1217	20 AAX99692	M13 DNA sequence u
4	1165.2	95.7	9955	9 AAN81542	Sequence of mcp1-2
5	1165.2	95.7	9955	11 AAQ05877	mgp1-2 plasmid seq
6	1165.2	95.7	9955	13 AAQ31625	Right-half vector
7	1150.8	94.6	7294	15 AAQ66626	Right-half vector
8	1150.8	94.6	7294	15 AAQ66630	M13IX421. Synthet
9	1147.6	94.3	7294	13 AAQ24174	

C 10	1144.4	94.0	7294	13	AAQ24170	M13IX42. Syntheti
C 11	1141	93.8	7300	22	AAF59234	M13mp18 nucleotide
C 12	1140.4	93.7	7084	21	AAZ51028	Modified filamento
C 13	1131.4	93.0	7317	19	AAV03651	M13-based vector M
C 14	1131.4	93.0	7317	20	AAZ16953	Plasmid M13IX11.
C 15	1131.4	93.0	7317	20	AAZ16953	Kappa light chain
C 16	1131.4	93.0	7320	15	AAQ66627	Left-half vector M
C 17	1131.4	93.0	7557	19	AAV03653	M13-based vector M
C 18	1131.4	93.0	7557	20	AAZ16961	Plasmid M13IX13.
C 19	1131.4	93.0	7557	21	AAZ91527	Nucleotide sequenc
C 20	1131.4	93.0	8118	19	AAV03654	M13-based vector M
C 21	1131.4	93.0	8118	21	AAZ91528	Plasmid M13IX60.
C 22	1131.4	93.0	7394	15	AAQ66631	Nucleotide sequenc
C 23	1131	92.9	7394	15	AAQ66629	Left-half vector M
C 24	1131	92.9	7409	15	AAQ66628	Vector M13IX30 for
C 25	1131	92.9	7445	15	AAQ66628	M13-based vector M
C 26	1131	92.9	7445	19	AAV03650	Plasmid M13IX30.
C 27	1131	92.9	7445	20	AAZ16937	Heavy chain Fd lib
C 28	1131	92.9	7445	21	AAZ91524	M13-based vector M
C 29	1131	92.9	7729	19	AAV03652	Plasmid M13IX34.
C 30	1131	92.9	7729	20	AAZ91526	Nucleotide sequenc
C 31	1131	92.9	7394	13	AAQ24175	M13ED04. Syntheti
C 32	1129.4	92.8	7394	13	AAQ24172	M13IX30. Syntheti
C 33	1126.2	92.5	7445	13	AAQ24172	M13IX22. Syntheti
C 34	1121.8	92.2	7320	13	AAQ24173	M13IXD03. Synthet
C 35	1121.4	92.1	7409	13	AAQ24173	M13mp18 sense stra
C 36	1030.4	84.7	1050	14	AAQ46689	Sequencing vector
C 37	846.8	69.6	7652	14	AAQ46682	Sequence of phage
C 38	754	62.0	6971	20	AAZ6304	Sequence of phage
C 39	739.6	60.8	7055	20	AAZ6303	Chimeric adeno-ass
C 40	739.6	60.8	7783	20	AAZ6302	Chimeric adeno-ass
C 41	716.4	58.9	8151	21	AAZ00832	Plasmid pAV CMVlac
C 42	716.4	58.9	8178	21	AAZ00834	AV.CMVlac2 cis pla
C 43	716.4	58.9	8509	18	AAZ59271	Second generation
C 44	716.4	58.9	8509	20	AAZ33862	
C 45	715.4	58.8	8299	18	AAZ59273	

ALIGNMENTS

RESULT 1
AAV12871 standard; DNA; 1217 BP.
XX AAV12871;
AC AAV12871;
DT 14-MAY-1998 (first entry)
DE M13 DNA sequence.

Energy transfer dye; donor dye; acceptor dye; oligonucleotide labelling;
nucleic acid sequencing; fluorescence intensity; M13; ss.
Synthetic.
XX EP805190-A2.
PN 05-NOV-1997.
XX 02-MAY-1997; 97EP-0303039.
XX 04-OCT-1996; 96US-0726462.
PR 03-MAY-1996; 96US-0642330.
XX (PEKE) PERKIN-ELMER CORP.
XX Lee LG, Rosenblum B, Spurgeon SL;
WPI; 1997-529051/49.
XX Fluorescent energy transfer dyes - useful for labelling
dideoxynucleotides, oligonucleotides, etc.

XX
XX

Example 5; Page 54-55; 79pp; English.

This sequence represents the M13 sequence identified using the primer shown in AAV12871 labelled with a dye of the invention. The dye is an energy transfer dye of formula D-R21-Z1-CO-R22-R28-A (1), where: D is a donor dye that absorbs light at a first wavelength and emits excitation energy in response; A is an acceptor dye that absorbs the excitation energy from D and fluoresces at a second wavelength in response; Z1 = NH, S or O; R21 = 1-5C alkylene; R22 = an alkene, diene or alkene group, an unsaturated 5- or 6-membered ring or a fused ring structure; R28 = a group which includes a functionality to attach the linker to the acceptor dye. R28 is especially R29-Z2-CO, where R29 = 1-5C alkylene and Z2 = NH, S or O. The dyes are used for labelling nucleosides, nucleoside mono-, di- and triphosphates, oligonucleotides and oligonucleotide analogues, especially for labelling oligonucleotide primers or didoxynucleotides used for nucleic acid sequencing. The dyes give greater fluorescence intensities than the acceptor dyes alone.

Sequence 1217 BP; 335 A; 291 C; 321 G; 270 T; 0 other;

Query Match 100.0%; Score 1217; DB 18; Length 1217;
Best Local Similarity 100.0%; Pred. No. 8.2e-221;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAAGCTTGCATGCGCTGAGGTCGACTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60
DB 1 GCCAAGCTTGCATGCGCTGAGGTCGACTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60
QY 61 GTAATCATGGTCATAGCTGTTCTCTGTGTGAATTTTATCCGCTCAGCAATTCACACAA 120
DB 61 GTAATCATGGTCATAGCTGTTCTCTGTGTGAATTTTATCCGCTCAGCAATTCACACAA 120
QY 121 CATAGAGCGCGAAGCATAAAGTGTAAAGCTGGGGTGCCTAATGAGTGAAGTAACTCAC 180
DB 121 CATAGAGCGCGAAGCATAAAGTGTAAAGCTGGGGTGCCTAATGAGTGAAGTAACTCAC 180
QY 181 ATTAATTCGGTTGCGCTCAGTCCCGCTTCCAGTCCGGAACCTGCTCGCAGCTGCA 240
DB 181 ATTAATTCGGTTGCGCTCAGTCCCGCTTCCAGTCCGGAACCTGCTCGCAGCTGCA 240
QY 241 TTAATGAATCGCCACCGCGGGGAGAGGGGTTGCTGTTGGCGCGCAGGGTGGTTT 300
DB 241 TTAATGAATCGCCACCGCGGGGAGAGGGGTTGCTGTTGGCGCGCAGGGTGGTTT 300
QY 301 TTCTTTTACACAGTGAAGCGGCAACAGCTGATTGCCCTTCCAGCTTGGCCCTGAGAGA 360
DB 301 TTCTTTTACACAGTGAAGCGGCAACAGCTGATTGCCCTTCCAGCTTGGCCCTGAGAGA 360
QY 361 GTTCAGCAGCGTCCAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
DB 361 GTTCAGCAGCGTCCAGCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
QY 421 TTCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGGTTGAGTGT 480
DB 421 TTCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGGTTGAGTGT 480
QY 481 TGTTCAGTTTGAACAGAGTCCACTATTAAAGAACGTGCTGCTGCTGCTGCTGCTGCTGCT 540
DB 481 TGTTCAGTTTGAACAGAGTCCACTATTAAAGAACGTGCTGCTGCTGCTGCTGCTGCTGCT 540
QY 541 AAAACCGCTTATCAGGCGGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
DB 541 AAAACCGCTTATCAGGCGGATGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 601 GGGGTGAGGTGCGGTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCCGATTTAGACC 660
DB 601 GGGGTGAGGTGCGGTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCCGATTTAGACC 660
QY 661 TTGACGGGAAAGCGGCGGAGTGGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
DB 661 TTGACGGGAAAGCGGCGGAGTGGCGGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720

QY 721 CGTAGGGCGCTGGCAAGTGTAGCGGTACAGGTGCGGCTAACCCACACACCCCGCGCT 780
DB 721 CGTAGGGCGCTGGCAAGTGTAGCGGTACAGGTGCGGCTAACCCACACACCCCGCGCT 780
QY 781 TAATGCGCGCTACAGGGCGGCTACTATGTTGCTTTTACGAGCAGCTATTAAGTGTGTTT 840
DB 781 TAATGCGCGCTACAGGGCGGCTACTATGTTGCTTTTACGAGCAGCTATTAAGTGTGTTT 840
QY 841 CCTGCTTGAATCAGAGCGGGAGCTAAACAGGAGCGGCTTAAAGGGATTTTACACAGGA 900
DB 841 CCTGCTTGAATCAGAGCGGGAGCTAAACAGGAGCGGCTTAAAGGGATTTTACACAGGA 900
QY 901 AGGTACGCCAGAACTCTTGAAGTGTGTTTATTAATCAGTGAAGGCGGCGGAGGAGGAGG 960
DB 901 AGGTACGCCAGAACTCTTGAAGTGTGTTTATTAATCAGTGAAGGCGGCGGAGGAGGAGG 960
QY 961 TCTGCTCATCAGCAAAATTAACCGTTGTAGCAATACTTCTTTGATTAGTAAATCAATCAC 1020
DB 961 TCTGCTCATCAGCAAAATTAACCGTTGTAGCAATACTTCTTTGATTAGTAAATCAATCAC 1020
QY 1021 TTGCTGCTAGTAGAAGAACTCAAACTATCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
DB 1021 TTGCTGCTAGTAGAAGAACTCAAACTATCGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080
QY 1081 CGCCAGCGCTTGCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
DB 1081 CGCCAGCGCTTGCACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1140
QY 1141 TCTGAAATGATTTTATCATTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
DB 1141 TCTGAAATGATTTTATCATTGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1200
QY 1201 CATTGCGGCAACAGAG 1217
DB 1201 CATTGCGGCAACAGAG 1217

RESULT 2

AAZ09714

ID AAZ09714 standard; DNA; 1217 BP.

AC AAZ09714;

XX 15-NOV-1999 (first entry)

DT Bacteriophage M13 DNA fragment.

DE Energy transfer dye; fluorescence; donor; acceptor; excitation energy;

DE Light absorption; nucleic acid sequencing; detection; fluorophore; ss.

KW Bacteriophage m13.

OS US5945526-A.

XX 31-AUG-1999.

PN 23-MAR-1998; 98US-0046203.

XX 23-MAR-1998; 98US-0046203.

PR 03-MAY-1996; 96US-0642330.

PR 27-JUN-1996; 96US-0672196.

XX (PEKE) PERKIN-ELMER CORP.

PI Lee LG, Rosenblum B, Spurgeon SL;

XX WPI; 1999-550120/46.

DR New energy transfer dye, used in nucleic acid sequencing

XX Disclosure; Column 85-88; 77pp; English.

PS

XX

Db	5223	AGAACAAATATTACCGCAGCCATTGCAACAGGAAAAAGCCTCATGGAATAACCTACATTT	5164
Qy	1128	TGACGCTCAATCGTCTGAATGGATTATTACATTTGGCAGATTCCACGACTCACAGACCA	1187
Db	5163	TGACGCTCAATCGTCTGAATGGATTATTACATTTGGCAGATTCCACGACTCACAGACCA	5104
Qy	1188	GTAATAAAGGGACATTTCTGGCCAAACAGAG	1217
Db	5103	GTAATAAAGGGACATTTCTGCCCAACAGAG	5074
RESULT 5			
AAQ05877/c	AAQ05877 standard; DNA; 9955 BP.		
XX	AAQ05877;		
XX	10-JAN-1991 (first entry)		
XX	mgp1-2 plasmid sequence encoding T7 RNA polymerase under the control		
DE	of a lac promoter.		
DE	pTrx-2; pGP5-5; mgp1-2; ds.		
KW	Bacteriophage t7.		
XX	EP386857-A.		
XX	12-SEP-1990.		
XX	24-DEC-1987; 87EP-0201138.		
XX	07-MAY-1990; 90EP-0201138.		
PR	14-JAN-1987; 87US-0003227.		
PR	14-DEC-1987; 87US-0132569.		
XX	(HARD) HARVARD COLLEGE.		
PA	Tabor S, Richardson CC;		
PI	WPI; 1990-276890/37.		
XX	Amplification of DNA sequences - by annealing primers then		
PT	incubating with T7-type DNA polymerase having reduced		
PT	exo:nuclease activity.		
XX	Example 1; Fig 9; 43pp; English.		
XX	In order to overproduce T7 DNA polymerase in a cellular expression		
CC	system, the two components, thioredoxin and gene 5 protein must be		
CC	produced in a one to one ratio.		
CC	Thioredoxin is cloned into plasmid pTrx-2 under the control of the		
CC	tac promoter.		
CC	T7 gene 5 is included in plasmid pGP5-5 under the control of the		
CC	phi 10 promoter.		
CC	Phi 10 promoter is induced only in the presence of T7 RNA polymerase		
CC	which is provided by the plasmid mgp1-2 under the influence of the		
CC	lac promoter.		
XX	Sequence 9955 BP; 2454 A; 2219 C; 2241 G; 3038 T; 3 other;		
SQ			
Query Match 95.7%; Score 1165.2; DB 11; Length 9955;			
Best Local Similarity 99.7%; Pred. No. 4.2e-211;			
Matches 1167; Conservative 0; Mismatches 3; Indels 0; Gaps 0;			
Qy	48	CGAGCTCGAATTCGTAATCATGCTGTTCCCTGCTGTAATTTGTAATTCGCTCA	107
Db	6243	CGAGCTCGAATTCGTAATCATGCTGTTCCCTGCTGTAATTTGTAATTCGCTCA	6184
Qy	108	CAATTCACACATACGAGCGGAGCATAAAGCTGTAAGCCCTGGGCTGCTAATGAG	167
Db	6183	CAATTCACACATACGAGCGGAGCATAAAGCTGTAAGCCCTGGGCTGCTAATGAG	6124
Qy	168	TGAGCTAATCTACATTAATTCGGTTGCGCTCACTGCCGCTTCCAGTCGGGAAACCTGT	227
Db	6123	TGAGGTAATCTACATTAATTCGGTTGCGCTCACTGCCGCTTCCAGTCGGGAAACCTGT	6064
Qy	228	CGTCCAGCTGCATTAATGAATCGGCCAAGCGGGGAGAGGGGTTGCGTATTGGGC	287
Db	6063	CGTCCAGCTGCATTAATGAATCGGCCAAGCGGGGAGAGGGGTTGCGTATTGGGC	6004
Qy	288	GCCAGGCTGTTTCTTTTCCAGCTGAGACGGGCAACAGCTGATGCCCTTCCACGCC	347
Db	6003	GCCAGGCTGTTTCTTTTCCAGCTGAGACGGGCAACAGCTGATGCCCTTCCACGCC	5944
Qy	348	TGGCCCTGAGAGAGTTGACGAGCGGTCACGCTGTTGCCCGACGAGCGGAAATCC	407
Db	5943	TGGCCCTGAGAGAGTTGACGAGCGGTCACGCTGTTGCCCGACGAGCGGAAATCC	5884
Qy	408	TGTTTATGTTGTTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCGAGA	467
Db	5883	TGTTTATGTTGTTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCGAGA	5824
Qy	468	TAGGTTGAGTGTGTTTCCAGTTTGGAAACAGAGTCCACTATTAAGAACGTTGGACTCA	527
Db	5823	TAGGTTGAGTGTGTTTCCAGTTTGGAAACAGAGTCCACTATTAAGAACGTTGGACTCA	5764
Qy	528	ACGTCAAGGGGGAACACCGCTATCAGGGCGATGGCCACTAGCTGAACCATCACCA	587
Db	5763	ACGTCAAGGGGGAACACCGCTATCAGGGCGATGGCCACTAGCTGAACCATCACCA	5704
Qy	588	AATCAAGTTTTCGGGTCGAGTGGCGTAAAGCACTAAATCGGAACCCCTAAAGGAGCC	647
Db	5703	AATCAAGTTTTCGGGTCGAGTGGCGTAAAGCACTAAATCGGAACCCCTAAAGGAGCC	5644
Qy	648	CCCGATTAGAGCTTGACGGGGAACCGCGCAACGTCGGAGAAAGGAGGGAAGAAAG	707
Db	5643	CCCGATTAGAGCTTGACGGGGAACCGCGCAACGTCGGCGAGAAAGGAGGGAAGAAAG	5584
Qy	708	CGAAGAGCGGGCGCTAGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCA	767
Db	5583	CGAAGAGCGGGCGCTAGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCA	5524
Qy	768	CACCGCGCGCTTAATGCGCGCTACAGGGCGCTACTATGTTGCTTACGAGCAGC	827
Db	5523	CACCGCGCGCTTAATGCGCGCTACAGGGCGCTACTATGTTGCTTACGAGCAGC	5464
Qy	828	TATAAGCTGCTTCTCTGTAATCAGAGCGGGAGCTAAACAGAGGCGGCTAAAGGG	887
Db	5463	TATAAGCTGCTTCTCTGTAATCAGAGCGGGAGCTAAACAGAGGCGGCTAAAGGG	5404
Qy	888	ATTTTATAGAGGAGCGGTACGCGCAATCTTGTAGAGTGTGTTTATATCATGAGGCA	947
Db	5403	ATTTTATAGAGGAGCGGTACGCGCAATCTTGTAGAGTGTGTTTATATCATGAGGCA	5344
Qy	948	CCGAGTAAAGAGTCTGTCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTA	1007
Db	5343	CCGAGTAAAGAGTCTGTCATCAGCAAAATTAACCGTTGTAGCAATCTCTTTGATTA	5284
Qy	1008	GTAATTAACATCACTTGCCTGAGTAGAAGAACTCAAACTATCGGCCTTGTGTAATACC	1067
Db	5283	GTAATTAACATCACTTGCCTGAGTAGAAGAACTCAAACTATCGGCCTTGTGTAATACC	5224
Qy	1068	AGAACAAATATTACCGCAGCCATTTGCAACAGGAAACCGCTCATGGAATACCTACATTT	1127

QY 408 TGTTGATGGTGGTTCGCAATCCGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGA 467
DB 5883 TGTTGATGGTGGTTCGCAATCCGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGA 5824
QY 468 TAGGTTGAGTGTGTTCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGACTCCA 527
DB 5823 TAGGTTGAGTGTGTTCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGACTCCA 5764
QY 528 ACGTCAAGGGGCAAAACCGCTATCAGGGCGATGGCCCACTAGTGAACCATCACCA 587
DB 5763 ACGTCAAGGGGCAAAACCGCTATCAGGGCGATGGCCCACTAGTGAACCATCACCA 5704
QY 588 ATCAAGTTTGTGGGTGAGGTCCGCTAAAGCACTAAATCGGAACCTTAAGGGAGCC 647
DB 5703 ATCAAGTTTGTGGGTGAGGTCCGCTAAAGCACTAAATCGGAACCTTAAGGGAGCC 5644
QY 648 CCGGATTTAGAGCTTGAGCGGGAAGCGCGGACGTGGCGAGAAGGAAGGGAAG 707
DB 5643 CCGGATTTAGAGCTTGAGCGGGAAGCGCGGACGTGGCGAGAAGGAAGGGAAG 5584
QY 708 CGAAGGAGCGGCGCTAGGCGCTGGCAAGTGTAGCGGTCACTGCGGTAAACCA 767
DB 5583 CGAAGGAGCGGCGCTAGGCGCTGGCAAGTGTAGCGGTCACTGCGGTAAACCA 5524
QY 768 CACCCCGCGCTTAATCGCCGCTACAGGGCGGTACTATGTTGCTTTGACGACG 827
DB 5523 CACCCCGCGCTTAATCGCCGCTACAGGGCGGTACTATGTTGCTTTGACGACG 5464
QY 828 TATAAGCTGTTTCCCTGTTGGATCAGAGCGGAGCTAAACAGAGGCGGATTAAGG 887
DB 5463 TATAAGCTGTTTCCCTGTTGGATCAGAGCGGAGCTAAACAGAGGCGGATTAAGG 5404
QY 888 ATTTTACAGAGGAGCGTACCGCAGAACTTTGAGAAGTGTGTTTATAATCAGTGAGGCA 947
DB 5403 ATTTTACAGAGGAGCGTACCGCAGAACTTTGAGAAGTGTGTTTATAATCAGTGAGGCA 5344
QY 948 CCGAGTAAAGAGTGTGTCATCAGCGAAATTAACCGTTGTAGCAATCTCTTTGATTA 1007
DB 5343 CCGAGTAAAGAGTGTGTCATCAGCGAAATTAACCGTTGTAGCAATCTCTTTGATTA 5284
QY 1008 GTAATACATCACTTGCCTGAGTAGAAGAACTCAAACTATCGGCTTTGCTGGTAATACC 1067
DB 5283 GTAATACATCACTTGCCTGAGTAGAAGAACTCAAACTATCGGCTTTGCTGGTAATACC 5224
QY 1068 AGAACAATATTACCGCCAGCCATTGCAACAGGAAACCGCTCATGGAAATACCTACATTT 1127
DB 5223 AGAACAATATTACCGCCAGCCATTGCAACAGGAAACCGCTCATGGAAATACCTACATTT 5164
QY 1128 TGAGCTCAATCGTCTGAATGGATTTATTTACATTTGGCAGATTCCACAGTCAACGACCA 1187
DB 5163 TGAGCTCAATCGTCTGAATGGATTTATTTACATTTGGCAGATTCCACAGTCAACGACCA 5104
QY 1188 GTAATAAAGGAGACATTTGCGCCACAGAG 1217
DB 5103 GTAATAAAGGAGACATTTGCGCCACAGAG 5074

RESULT 7
ID AAQ66626/c
XX AAQ66626 standard; DNA; 7294 BP.
AC AAQ66626;
XX
DT 20-JAN-1995 (first entry)
XX
DE Right-half vector M13IX42.
XX
KW vector M13IX42; right-half vector; randomised oligonucleotides;
KW surface expression; random peptide; constrained secondary structure;
KW pseudo wild-type M13 gene VIII; ds.
XX
OS Synthetic.

XX WO9411496-A.
XX 26-MAY-1994.
XX 09-NOV-1993; 93WO-US10850.
XX 10-NOV-1992; 92US-0978893.
XX (IXSY-) IXSYS INC.
XX Huse WD;
XX WPI; 1994-183498/22.
XX Cells expressing oligo:nucleotide(s) having random codon
XX sequences - are used for producing soluble peptide(s) having a
XX constrained secondary structure in soln..
XX Example 1: Page 78-82; 152pp; English.
XX M13IX42 was constructed to harbour the right-half populations of
XX randomised oligonucleotides. M13mp8 was the starting vector which
XX was modified to contain, in addition to the encoded wild-type M13
XX gene VIII all ready present in the vector: a pseudo-wild-type M13
XX gene VIII sequence with a stop codon placed between it and an EcoRI-
XX SacI cloning site for randomised oligonucleotides; a pair of PstI
XX sites to be used for joining with M13IX22, the left-hand vector; a
XX second stop codon placed on the opposite side of the vector than the
XX portion being combined with the left-half vector; and various other
XX mutations to remove redundant restriction sites and the N-terminal
XX portion of LacZ.
XX Sequence 7294 BP; 1787 A; 1528 C; 1552 G; 2427 T; 0 other;
SQ

Query Match 94.6%; Score 1150.8; DB 15; Length 7294;
Best Local Similarity 99.8%; Pred. No. 2.2e-208; Indels 0; Gaps 0;
Matches 1152; Conservative 0; Mismatches 2;
QY 64 ATCATGTCATAGCTGTTTCCCTGTGTAATTTGTAATGCTTATCGCTCACAATTTCCACACAACT 123
DB 6226 ATCTGTCATAGCTGTTTCCCTGTGTAATTTGTAATGCTTATCGCTCACAATTTCCACACAACT 6167
QY 124 ACGAGCGGAAGCATAAAGTGTAAAGCTTGTGTAATTTGTAATGCTTATCGCTCACAATTTCCACACAACT 183
DB 6166 ACGAGCGGAAGCATAAAGTGTAAAGCTTGTGTAATTTGTAATGCTTATCGCTCACAATTTCCACACAACT 6107
QY 184 AATTGCTTGCCTGCTACTGCGCTTTTCCAGTCGGGAAACCTTCTGTCGAGCTGCATTA 243
DB 6106 AATTGCTTGCCTGCTACTGCGCTTTTCCAGTCGGGAAACCTTCTGTCGAGCTGCATTA 6047
QY 244 ATGAATCGGCAACGCGCGGGAGAGCGGTTTGGCGTATTTGGCGCCAGGCTGTTTTC 303
DB 6046 ATGAATCGGCAACGCGCGGGAGAGCGGTTTGGCGTATTTGGCGCCAGGCTGTTTTC 5987
QY 304 TTTTCACAGTGAGACGCGGAACAGCTGATTGCCCTTTCAGCGCTGCGCCCTGAGAGAGTT 363
DB 5986 TTTTCACAGTGAGACGCGGCAACAGCTGATTGCCCTTTCAGCGCTGCGCCCTGAGAGAGTT 5927
QY 364 GCAGCAAGCGGTCCACGCTGTTTGGCCCGAGCAGCGGAAATCTCTGTTGATGTTGTTTC 423
DB 5926 GCAGCAAGCGGTCCACGCTGTTTGGCCCGAGCAGCGGAAATCTCTGTTGATGTTGTTTC 5867
QY 424 CGAATCGGCAAAATCTCTTATAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 483
DB 5866 CGAATCGGCAAAATCTCTTATAATCAAAAGATAGCCCGAGATAGGTTGAGTGTGT 5807
QY 484 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGAGCTCCAACTCCAAAGGCGGAAA 543
DB 5806 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGAGCTCCAACTCCAAAGGCGGAAA 5747
QY 544 AACCGCTCTATAGCGCGGATGCGCCCACTACGTTGAACCATTCACCCAAATCAAGTTTTTTGGG 603

Db 5746 AACCGTCTACAGGGCGATGCCCCACCTACGTGAACCATCACCCAAATCAAGTCTTTTGGG 5687
 QY 604 GTCAGGTGCGGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCGCCGATTTAGAGCTTG 663
 Db 5686 GTCAGGTGCGGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCGCCGATTTAGAGCTTG 5627
 QY 664 ACAGGGAAAGCCGCGAAGCTGGCGAGAAAGGAAGGAAGAAAGCAAGAGAGGGGGCGC 723
 Db 5626 ACAGGGAAAGCCGCGAAGCTGGCGAGAAAGGAAGGAAGGAAGCAAGAGAGGGGGCGC 5567
 QY 724 TAGGGCGCTGCAAGTGTAGCGGTGACGCTGCGCGTAAACACACACACCCCGCGCTTAA 783
 Db 5566 TAGGGCGCTGCAAGTGTAGCGGTGACGCTGCGCGTAAACACACACACCCCGCGCTTAA 5507
 QY 784 TGCGCGCTACAGGGCGGTACTATGCTTTGAGGAGCAGCAGTATAACGCTGCTTCCCT 843
 Db 5506 TGCGCGCTACAGGGCGGTACTATGCTTTGAGGAGCAGCAGTATAACGCTGCTTCCCT 5447
 QY 844 CGTTGGAATCAGAGCGGGAGCTAAACAGAGGCGCGATTAAGGGATTTAGACAGGAACG 903
 Db 5446 CGTTGGAATCAGAGCGGGAGCTAAACAGAGGCGCGATTAAGGGATTTAGACAGGAACG 5387
 QY 904 GTAGCGCAGATCTTGAAGTGTGTTTATATACAGTGAAGGCGCGATTAAGGGATTTAGACAGGAACG 963
 Db 5386 GTAGCGCAGATCTTGAAGTGTGTTTATATACAGTGAAGGCGCGATTAAGGGATTTAGACAGGAACG 5327
 QY 964 GTCCATCAGCAAAATTAACCGTGTAGCAATACTCTTTGATTTAGTAATACATCACTTG 1023
 Db 5326 GTCCATCAGCAAAATTAACCGTGTAGCAATACTCTTTGATTTAGTAATACATCACTTG 5367
 QY 1024 CTGAGTAGAAGCACTCAAACTATGCGCCTTGTGCTGTAATATCCAGCAAAATTAACCGC 1083
 Db 5266 CTGAGTAGAAGCACTCAAACTATGCGCCTTGTGCTGTAATATCCAGCAAAATTAACCGC 5207
 QY 1084 CAGCCATTGCAACAGGAAGCACTGAGCAATACCTTACATTTTACGCTCAATCGCT 1143
 Db 5206 CAGCCATTGCAACAGGAAGCACTGAGCAATACCTTACATTTTACGCTCAATCGCT 5147
 QY 1144 GAAATGGATTTTACATTTGGCAGATTCACAGTCAACAGCAGCAGTAAAGGGAGCAT 1203
 Db 5146 GAAATGGATTTTACATTTGGCAGATTCACAGTCAACAGCAGCAGTAAAGGGAGCAT 5087
 QY 1204 TCTGCCCAACAGAG 1217
 Db 5086 TCTGCCCAACAGAG 5073

RESULT 8
 ID AAQ66630/c
 AC AAQ66630; standard; DNA; 7294 BP.
 AC AAQ66630;
 XX 23-JAN-1995 (first entry)
 DE Right-half vector M13IX421.
 XX vector M13IX421; right-half vector; randomised oligonucleotides;
 KW surface expression; random peptide; constrained secondary structure;
 KW pseudo wild-type M13 gene VIII; ds.
 XX Synthetic.
 OS
 XX WO9411496-A.
 PN
 PD 26-MAY-1994.
 XX
 PF 09-NOV-1993; 93WO-US10850.
 XX
 PR 10-NOV-1992; 92US-0978893.
 XX
 PA (IXSY-) IXSYS INC.

XX Huse WD;
 XX WPI; 1994-183498/22.
 XX Cells expressing oligo:nucleotide(s) having random codon
 PT sequences - are used for producing soluble peptide(s) having a
 PT constrained secondary structure in soln.
 XX Example 3; Page 94-97; 152pp; English.
 PS
 XX M13IX421 is identical to vector M13IX42 (AAQ66626) except that the
 CC amber codon between the EcoRI-SacI cloning site and the pseudo-wild
 CC type gene VIII sequence was removed. This change ensures that all
 CC expression off the lacZ promoter produces a peptide-gene VIII
 CC fusion protein. The vector was used for the construction of right
 CC half oligonucleotide libraries.
 XX
 SQ Sequence 7294 BP; 1787 A; 1528 C; 1553 G; 2426 T; 0 other;

Query Match 94.6%; Score 1150.8; DB 15; Length 7294;
 Best Local Similarity 99.8%; Pred. No. 2.2e-208;
 Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 64 ATCATGTGTCATAGCTGTTCTCTGTGTGAATTTGTATTCGGCTCAAAATTCACACAACAT 123
 Db 6226 ATCTGTGTCATAGCTGTTCTCTGTGTGAATTTGTATTCGGCTCAAAATTCACACAACAT 6167
 QY 124 ACAGGCGGAAAGCAATAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGCTAACTCACAAT 183
 Db 6166 ACAGGCGGAAAGCAATAAGTGTAAAGCTTGGGTGCTTAATGAGTGAGCTAACTCACAAT 6107
 QY 184 AATTGGCTTCCGCTCACTGCTGCTTTCAGTCTGGGAAACCTGTCTGCTGCCAGCTGCAATTA 243
 Db 6106 AATTGGCTTCCGCTCACTGCTGCTTTCAGTCTGGGAAACCTGTCTGCTGCCAGCTGCAATTA 6047
 QY 244 ATGAATCGGCAACACGCGGGGAGAGCGGTTTTCGCTATTTGGGCGCCAGAGTGGTTTTC 303
 Db 6046 ATGAATCGGCAACACGCGGGGAGAGCGGTTTTCGCTATTTGGGCGCCAGAGTGGTTTTC 5987
 QY 304 TTTTACACAGTGAAGCGGCAACAGCTGATTTGCCCTTACCGCTTGGCCCTTGAGAGAGTT 363
 Db 5986 TTTTACACAGTGAAGCGGCAACAGCTGATTTGCCCTTACCGCTTGGCCCTTGAGAGAGTT 5927
 QY 364 GCAGCAAGCGTCCACGCTGTTTCCCGCAGCAGCGGAAATCCTGTTGATGGTGGTTC 423
 Db 5926 GCAGCAAGCGTCCACGCTGTTTCCCGCAGCAGCGGAAATCCTGTTGATGGTGGTTC 5867
 QY 424 CGAAATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGTTGAGTGTGT 483
 Db 5866 CGAAATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGTTGAGTGTGT 5807
 QY 484 TCCAGTTTGGAAACAAGAGTCCCACTATTAAGAACGTTGGACTCCAAGCTCAAAAGGGCGAA 543
 Db 5806 TCCAGTTTGGAAACAAGAGTCCCACTATTAAGAACGTTGGACTCCAAGCTCAAAAGGGCGAA 5747
 QY 544 AACCGTCTATCAGGGCGATGGCCCACTACGTGAAGCAATCACCCAAATCAAGTTTGGG 603
 Db 5746 AACCGTCTATCAGGGCGATGGCCCACTACGTGAAGCAATCACCCAAATCAAGTTTGGG 5687
 QY 604 GTCAGGTGCGGTAAAGCACTAAATTCGGAACCCCTAAAGGGAGCCGCCGATTTAGAGCTTG 663
 Db 5686 GTCAGGTGCGGTAAAGCACTAAATTCGGAACCCCTAAAGGGAGCCGCCGATTTAGAGCTTG 5627
 QY 664 ACAGGGAAAGCCGCGAAGCTGGCGAGAAAGGAAGGAAGGAAGCAAGAGAGGGGGCGC 723
 Db 5626 ACAGGGAAAGCCGCGAAGCTGGCGAGAAAGGAAGGAAGGAAGCAAGAGAGGGGGCGC 5567
 QY 724 TAGGGCGCTGCAAGTGTAGCGGTGACGCTGCGGCTAACACACACACCCCGCGCTTAA 783
 Db 5566 TAGGGCGCTGCAAGTGTAGCGGTGACGCTGCGGCTAACACACACACCCCGCGCTTAA 5507

CC elements and to gVIII. These vectors encode a pseudo-wild type gVIII product. This gene encodes the wild-type M13 gVIII amino acid sequence but has been changed at the nucleotide level to reduce homologous recombination with the wild-type gVIII contained on these vectors. The wild-type gVIII is present to ensure that at least some functional, non-fusion coat protein is produced. They also contain the expression elements for the peptide fusion proteins. A ribosome binding site and LacZ promoter/operator elements are present for transcription and translation of the peptide fusion proteins. Various restriction sites are present for the cloning of random peptides.

XX
SQ Sequence 7294 BP; 1796 A; 1527 C; 1553 G; 2418 T; 0 other;

Query Match 94.3%; Score 1147.6; DB 13; Length 7294;
Best Local Similarity 99.7%; Pred. No. 8.8e-208;
Matches 1150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 784 TGGCGCGTACAGGCGGCTACTATGTTGCTTTGACGACGCTATAACGTTGCTTTCCT 843
DB 5506 TGGCGCGTACAGGCGGCTACTATGTTGCTTTGACGAGCAGCTATAACGTTGCTTTCCT 5447
QY 844 CGTTGGAATCAGAGCGGAGCTAAACAGAGGCGCGATTAAAGGATTTCACAGGAACG 903
DB 5446 CGTTGGAATCAGAGCGGAGCTAAACAGAGGCGCGATTAAAGGATTTCACAGGAACG 5387
QY 904 GTACGCCAGAAATCTTGAGAAATGTTTATTAATCAGTGGAGCCACCGAGTAAAGAGTCT 963
DB 5386 GTACGCCAGAAATCTTGAGAAATGTTTATTAATCAGTGGAGCCACCGAGTAAAGAGTCT 5327
QY 964 GTCCATCAGCAAAATTAACCGTTGAGCAATACCTTCTTTGATTAGTAATACATCATCTTG 1023
DB 5326 GTCCATCAGCAAAATTAACCGTTGAGCAATACCTTCTTTGATTAGTAATACATCATCTTG 5267
QY 1024 CCGTGTAGAGAACTCAAACTATCGGCTTCTGCTGATATCCAGACAATATTAACCGC 1083
DB 5266 CCGTGTAGAGAACTCAAACTATCGGCTTCTGCTGATATCCAGACAATATTAACCGC 5207
QY 1084 CAGCCATTGCAAGAAACGCTCATGGAATACCTACATTTTGAAGCTCAATCGTCT 1143
DB 5206 CAGCCATTGCAAGAAACGCTCATGGAATACCTACATTTTGAAGCTCAATCGTCT 5147
QY 1144 GAAATGCAATATTACATTTGGCAGATTCCAGCTCACAGCACAGTAATAAAGGACAT 1203
DB 5146 GAAATGCAATATTACATTTGGCAGATTCCAGCTCACAGCACAGTAATAAAGGACAT 5087
QY 1204 TCTGGCCACAGAG 1217
DB 5086 TCTGGCCACAGAG 5073

RESULT 9
ID AAQ24174/c
XX AAQ24174;
XX 19-JAN-1993 (first entry)
XX M13X421.
XX M13; cloning vectors; gVIII; pseudo-wild type; coat protein; RBS;
XX LacZ; ss.
XX Synthetic.
XX WO9206176-A.
XX 16-APR-1992.
XX 27-SEP-1991; 91WO-US07141.
XX 28-SEP-1990; 90US-0590664.
XX (IXSY-) IXSYS INC.
XX Huse WD;
XX WPI; 1992-150863/18.
XX Surface expression libraries of randomised peptide(s) -
XX comprising vectors contg. diverse populations of
XX oligonucleotide(s) having desirable bias of random codon
XX sequences
XX Disclosure; Page 85-88; 142pp; English.
XX The sequences given in AAQ24173-5 are vectors which allow the expression
XX of random peptides on the surface of M13. The vectors are produced by
XX combining separate vectors into a single larger vector. This system
XX produces random oligonucleotides functionally linked to expression

CC elements and to gVIII. These vectors encode a pseudo-wild type gVIII product. This gene encodes the wild-type M13 gVIII amino acid sequence but has been changed at the nucleotide level to reduce homologous recombination with the wild-type gVIII contained on these vectors. The wild-type gVIII is present to ensure that at least some functional, non-fusion coat protein is produced. They also contain the expression elements for the peptide fusion proteins. A ribosome binding site and LacZ promoter/operator elements are present for transcription and translation of the peptide fusion proteins. Various restriction sites are present for the cloning of random peptides.

XX
SQ Sequence 7294 BP; 1796 A; 1527 C; 1553 G; 2418 T; 0 other;

Query Match 94.3%; Score 1147.6; DB 13; Length 7294;
Best Local Similarity 99.7%; Pred. No. 8.8e-208;
Matches 1150; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 64 ATCATGTTATAGCTGTTTCTGTTGAAATTTGTTATCCGCTCACAATTCACACACAT 123
DB 6226 ATCTGTTATAGCTGTTTCTGTTGAAATTTGTTATCCGCTCACAATTCACACACAT 6167
QY 124 ACGAGCGGAAGCATAAAGCTGTAAAGCTGGGTGCTTAATGAGTGAGCTAACTCAGATT 183
DB 6166 ACGAGCGGAAGCATAAAGCTGTAAAGCTGGGTGCTTAATGAGTGAGCTAACTCAGATT 6107
QY 184 AATTCGTTGCGCTCACTGCGCGCTTCCAGTCGGGAAACCTGCTGCCAGCTCATTA 243
DB 6106 AATTCGTTGCGCTCACTGCGCGCTTCCAGTCGGGAAACCTGCTGCCAGCTCATTA 6047
QY 244 ATGAATTCGGCCAAACGCGGGGAGAGCGGTTTGGGTATTTGGGCGCAGGTTTTC 303
DB 6046 ATGAATTCGGCCAAACGCGGGGAGAGCGGTTTGGGTATTTGGGCGCAGGTTTTC 5987
QY 304 TTTTCACAGTGTAGAGCGGCAACAGCTGATTCCTTACCCGCTGGCCCTGAGAGATT 363
DB 5986 TTTTCACAGTGTAGAGCGGCAACAGCTGATTCCTTACCCGCTGGCCCTGAGAGATT 5927
QY 364 GCAGCAAGCGGTTCCAGCTGTTTGGCCAGCAGCGGAAATCTCTTTGATGTTGTTTC 423
DB 5926 GCAGCAAGCGGTTCCAGCTGTTTGGCCAGCAGCGGAAATCTCTTTGATGTTGTTTC 5867
QY 424 CGAAATTCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGATAGGTTGAGTTGT 483
DB 5866 CGAAATTCGCAAAATCCCTTATAAATCAAAAGAAATAGCCGATAGGTTGAGTTGT 5807
QY 484 TCCAGTTTGGCAACAAGAGTCCACTATTAAGAAGCTGGAGTCCAGCTCAAGCGGCGAAA 543
DB 5806 TCCAGTTTGGCAACAAGAGTCCACTATTAAGAAGCTGGAGTCCAGCTCAAGCGGCGAAA 5747
QY 544 AACCGTCTATCAGGCGGATGCGCCACTACCTGAACCATACCCAAATCAAGTTTTCGG 603
DB 5746 AACCGTCTATCAGGCGGATGCGCCACTACCTGAACCATACCCAAATCAAGTTTTCGG 5687
QY 604 GTCGAGTGCCTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCCGATTTAGAGCTTG 663
DB 5686 GTCGAGTGCCTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCCGATTTAGAGCTTG 5627
QY 664 ACGGGGAAAGCGCGGCAACGTTGGCGGAAGAGGAGGAAAGGAGGAGCGGCGC 723
DB 5626 ACGGGGAAAGCGCGGCAACGTTGGCGGAAGAGGAGGAGGAGGAGGAGCGGCGC 5567
QY 724 TAGGCGCTGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCCGCGCTTAA 783
DB 5566 TAGGCGCTGCGTGTAGTGTAGCGGTACGCTGCGGTAAACCAACACCCCGCGCTTAA 5507
QY 784 TCGCGCGCTACAGGCGCGTACTATGTTGTTTTCAGCAGCAGTATACGTTCTTCT 843
DB 5506 TCGCGCGCTACAGGCGCGTACTATGTTGTTTTCAGCAGCAGTATACGTTCTTCT 5447
QY 844 CTTTGAATCAGAGCGGAGCTAAACAGAGCGGCTTAAAGGATTTTAGACAGGAACG 903
DB 5446 CTTTGAATCAGAGCGGAGCTAAACAGAGCGGCTTAAAGGATTTTAGACAGGAACG 5387

QY 904 GTAGCCAGAAATCTTGAGAGCTGTTTTTATATCAGTCAGGCCACCGAGTAAAGAGTCT 963
 Db 5386 GTAGCCAGAAATCTTGAGAGCTGTTTTTATATCAGTCAGGCCACCGAGTAAAGAGTCT 5327
 QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAATAACATCATTG 1023
 Db 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAATAACATCATTG 5267
 QY 1024 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGTTGTAATATCCAGACATATATACGGC 1083
 Db 5266 CTTGAGTAGAAGAACTCAAACTATCGGCTTGTGTTGTAATATCCAGACATATATACGGC 5207
 QY 1084 CAGCCATTGCAACAGGAAACGCTCATGGAATPACCTACATTTTGACGCTCAATCGTCT 1143
 Db 5206 CAGCCATTGCAACAGGAAACGCTCATGGAATPACCTACATTTTGACGCTCAATCGTCT 5147
 QY 1144 GAAATGGATTATTTACATTTGGCAGATTCACCACTCACACACAGTAAATAAGGGACAT 1203
 Db 5146 GAAATGGATTATTTACATTTGGCAGATTCACCACTCACACACAGTAAATAAGGGACAT 5087
 QY 1204 TCTGGCCACAGAG 1217
 Db 5086 TCTGGCCACAGAG 5073

RESULT 10 AAQ24170/c

ID AAQ24170 standard; DNA; 7294 BP.

AC AAQ24170;

XX 19-JAN-1993 (first entry)

DE M13IX42.

XX M13; cloning vectors; gVIII; M13IX22; M13IX30; pseudo-wild type;
 KW coat protein; RBS; ss.

XX Synthetic.

XX WO9206176-A.

PD 16-APR-1992.

XX 27-SEP-1991; 91WO-US07141.

XX 28-SEP-1990; 90US-0590664.

XX (IXSY-) IXSYS INC.

XX Huse WD;

DR WPI; 1992-150863/18.

XX Surface expression libraries of randomised peptide(s) -
 PT comprising vectors contg. diverse populations of
 PT oligonucleotide(s) having desirable bias of random codon
 XX sequences

PS Disclosure; Fig 5; 142pp; English.

XX The sequences given in AAQ24170-2 are vectors which allow the
 CC expression of random peptides on the surface of M13. The vectors
 CC are produced by combining separate vectors into a single larger
 CC vector. This system produces random oligonucleotides functionally
 CC linked to expression elements and to gVIII. M13IX42 is used for
 CC sense strand oligonucleotide portions. It encodes a pseudo-wild type
 CC gVIII product. This gene encodes the wild-type M13 gVIII amino acid
 CC sequence but has been changed at the nucleotide level to reduce
 CC homologous recombination with the wild-type gVIII contained on the
 CC same vector. The wild-type gVIII is present to ensure that at least
 CC some functional, non-fusion coat protein is produced. M13IX22 is used

CC for anti-sense strand oligonucleotide portions. It contains the
 CC expression elements for the peptide fusion proteins. A ribosome
 CC binding site and lacZ promoter/operator elements are present for
 CC transcription and translation of the peptide fusion proteins. M13IX30
 CC contains a wild-type and pseudo-wild-type gVIII genes and various
 XX restriction sites for cloning of random peptides.

SQ Sequence 7294 BP; 1789 A; 1525 C; 1554 G; 2426 T; 0 other;

Query Match 94.0%; Score 1144.4; DB 13; Length 7294;
 Best Local Similarity 99.5%; Pred. No. 3.5e-207;
 Matches 1148; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 64 ATCATGTGTCATAGCTGTTTCCCTGCTGAAATGTTATCCGTCACAAATTCACACAAAT 123
 Db 6226 ATCTGCTCATAGCTGTTTCCCTGCTGAAATGTTATCCGTCACAAATTCACACAAAT 6167
 QY 124 ACAGAGCCGGAAGCATAAAGTCTAAAGCTGGGGTCCCTAAAGTCTGAGTAACTCACATT 183
 Db 6166 ACAGAGCCGGAAGCATAAAGTCTAAAGCTGGGGTCCCTAAAGTCTGAGTAACTCACATT 6107
 QY 184 AATTGCGTTGCGCTCACTGCGGCTTCCAGTCGGGAAACCTGCTGCCAGCTCATTA 243
 Db 6106 AATTGCGTTGCGCTCACTGCGGCTTCCAGTCGGGAAACCTGCTGCCAGCTCATTA 6047
 QY 244 ATGNAATCGGCAACGCGCGGGAGAGCGGTTTCCGTATTGGGCCAGGGTGGTTC 303
 Db 6046 ATGNAATCGGCAACGCGCGGGAGAGCGGTTTCCGTATTGGGCCAGGGTGGTTC 5987
 QY 304 TTTTACCAGCTGAGACGGGCAACAGCTGATTGCGCTTACCGCTGGCCCTGAGAGATT 363
 Db 5986 TTTTACCAGCTGAGACGGGCAACAGCTGATTGCGCTTACCGCTGGCCCTGAGAGATT 5927
 QY 364 GCAGCAAGCGGTCACGCTGTTTGGCCAGAGCGGCAAAATCCTGTTGATGTTGTTTC 423
 Db 5926 GCAGCAAGCGGTCACGCTGTTTGGCCAGAGCGGCAAAATCCTGTTGATGTTGTTTC 5867
 QY 424 CGAAATCGGCAAAATCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGATGTTGT 483
 Db 5866 CGAAATCGGCAAAATCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGATGTTGT 5807
 QY 484 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTTGGACTCCAAACGTCAAAGGGCGAAA 543
 Db 5806 TCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTTGGACTCCAAACGTCAAAGGGCGAAA 5747
 QY 544 AACCGTCTATAGGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGGG 603
 Db 5746 AACCGTCTATAGGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTTGGG 5687
 QY 604 CTCGAGTGCCGTAAGACACTAAATCGGAACCTTAAGGAGCGCCCGGATTTAGAGCTTG 663
 Db 5686 CTCGAGTGCCGTAAGACACTAAATCGGAACCTTAAGGAGCGCCCGGATTTAGAGCTTG 5627
 QY 664 ACGGGAAAGCGCGGACGTCGGCGAAGGAAGGAAGGAAAGGAGGAGCGCGCG 723
 Db 5626 ACGGGAAAGCGCGGACGTCGGCGAAGGAAGGAAGGAAAGGAGGAGCGCGCG 5567
 QY 724 TAGGCGCTGGCAAGTGTAGCGGTACGCTGCCGCTAACCCACACACCGCGCGCTTAA 783
 Db 5566 TAGGCGCTGGCAAGTGTAGCGGTACGCTGCCGCTAACCCACACACCGCGCGCTTAA 5507
 QY 784 TGGCCCGCTACAGGCGCGTACTATGTTGCTTTCACGAGCAGTATACGTCGTTTCCT 843
 Db 5506 TGGCCCGCTACAGGCGCGTACTATGTTGCTTTCACGAGCAGTATACGTCGTTTCCT 5447
 QY 844 CGTTGGATCAGACGGGAGCTAAACAGAGCGCGGATTTAAAGGGATTTTAGACGAAGC 903
 Db 5446 CGTTGGATCAGACGGGAGCTAAACAGAGCGCGGATTTAAAGGGATTTTAGACGAAGC 5387
 QY 904 GTACGCGAGAAATCTTGAGAGTGTGTTTATATCAGTCAGGCGCCAGCTAAAGAGTCT 963
 Db 5386 GTACGCGAGAAATCTTGAGAGTGTGTTTATATCAGTCAGGCGCCAGCTAAAGAGTCT 5327

CC exemplification of the present invention.

QY 964 GTCCATCAGCAAAATTAACCGTTGTAGCAATACCTCTTTTGTATTACTAATAACATCACCTTG 1023
 XX
 Db 5326 GTCCATCAGCAAAATTAACCGTTGTAGCAATACCTCTTTTGTATTACTAATAACATCACCTTG 5267
 QY 1024 CCTGAGTAGAAGAACTCAAACTATCGGCTTGTCTGGTAAATATCCAGACAAATATTACCGC 1083
 Db 5266 CCTGAGTAGAAGAACTCAAACTATCGGCTTGTCTGGTAAATATCCAGACAAATATTACCGC 5207
 QY 1084 CAGCCATTGCAACAGAAAGGCTCATGGAATACCTACATTTTGACGCTCAATCGTCT 1143
 Db 5206 CAGCCATTGCAACAGAAAGGCTCATGGAATACCTACATTTTGACGCTCAATCGTCT 5147
 QY 1144 GAAATGGATTATTTACATTTGGCAGATTACCACTAGTCACAGCAGCAGTAATAAAGGACAT 1203
 Db 5146 GAAATGGATTATTTACATTTGGCAGATTACCACTAGTCACAGCAGCAGTAATAAAGGACAT 5087
 QY 1204 TCTGGCCCAACAGAG 1217
 Db 5086 TCTGGCCCAACAGAG 5073

RESULT 11

AAF59234/c
 ID AAF59234 standard; DNA: 7300 BP.

AC AAF59234;

DT 26-APR-2001 (first entry)

DE M13mp18 nucleotide sequence.

KW M13mp18; living organism; dead organism; nucleic acid copying;

KW isostatic condition; temperature; buffer; ionic strength; ds.

XX Bacteriophage M13.

XX US2001000077-A1.

XX 29-MAR-2001.

XX 30-NOV-2000; 2000US-0727349.

XX 03-FEB-1998; 98US-0302818.

XX (ENGE/) ENGELHARDT D L.

PA (STAV/) STAVRIANPOULOS J G.

PA (RABB/) RABBANI E.

PA (DONE/) DONEGAN J J.

XX Engelhardt DL, Stavrianopoulos JG, Rabbani E, Donegan JJ;

XX WPI; 2001-202468/20.

XX Producing copies of specific nucleic acids in vitro, without the need
 CC of intermediate structures, useful for determining if samples have come
 CC from living or dead organisms -

XX Disclosure; Fig 5: 4lpp; English.

XX The present invention describes a method for producing, in vitro, copies
 CC of a specific nucleic acid. The process does not require the use of
 CC intermediate structures for the production of the nucleic acid. The
 CC method comprises: (a) providing a nucleic acid sample containing the
 CC specific sequence; (b) contacting the sample with a mixture containing:
 CC (i) nucleic acid precursors; (ii) specific nucleic acid primers, each
 CC complementary to a distinct region of the sequence; and (iii) a nucleic
 CC acid producing catalyst; and (c) allowing the mixture to react under
 CC isostatic conditions of temperature, buffer and ionic strength. The
 CC method can be used for producing copies of specific nucleic acids in
 CC vitro. The process can be used to determine if a specific target
 CC nucleic acid was derived from a living or deceased organism. The present
 CC sequence represents a M13mp18 nucleotide sequence which is given in the

QY 1 GCCAAGCTTGCATCGCTGACAGTGCAGTCTAGAGGATCCCGGGTACGAGCTGAATTC 60
 Db 6390 GCCAAGCTTGCATCGCTGACAGTGCAGTCTAGAGGATCCCGGGTACGAGCTGAATTC 6331
 QY 61 GTAATCATGTCTAGCTGTTTCTGTGTGAAATTTTATCCGTCAAAATTCACACAA 120
 Db 6330 GTAATCATGTCTAGCTGTTTCTGTGTGAAATTTTATCCGTCAAAATTCACACAA 6271
 QY 121 CATACGAGCCGGAAGCAATAAGTGTAAAGCTGGGGTCCCTAATGAGTGACCTACTCAC 180
 Db 6270 CATACGAGCCGGAAGCAATAAGTGTAAAGCTGGGGTCCCTAATGAGTGACCTACTCAC 6211
 QY 181 ATTAATTTGCTTGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCTGCCAGCTGCA 240
 Db 6210 ATTAATTTGCTTGGCTCACTGCCCGCTTTCCAGTCGGGAAACCTGTCTGCCAGCTGCA 6151
 QY 241 TTAATGAATCGGCAACGCGCGGAGAGCGGTTTTCGTATTGGGCCGCCAGGGTGGTTT 300
 Db 6150 TTAATGAATCGGCAACGCGCGGAGAGCGGTTTTCGTATTGGGCCGCCAGGGTGGTTT 6091
 QY 301 TTCTTTTACCAGTGAGACGGGCAACAGCTGATTTGCCCTTACCAGCTGAGAGA 360
 Db 6090 TTCTTTTACCAGTGAGACGGGCAACAGCTGATTTGCCCTTACCAGCTGAGAGA 6031
 QY 361 GTTCAGCAACGGTCCACAGCTGTTTCCGCCAGCAGCGGAAATCTCTTTGATGGTGG 420
 Db 6030 GTTCAGCAACGGTCCACAGCTGTTTCCGCCAGCAGCGGAAATCTCTTTGATGGTGG 5971
 QY 421 TTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGT 480
 Db 5970 TTCCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGT 5911
 QY 481 TGTTCAGTTTGGCAACAGAGTCCCACTATTAAAGAACGTTGGACTCCAACGCTCAAGGGGG 540
 Db 5910 TGTTCAGTTTGGCAACAGAGTCCCACTATTAAAGAACGTTGGACTCCAACGCTCAAGGGGG 5851
 QY 541 AAAAACCGCTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTT 600
 Db 5850 AAAAACCGCTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTT 5791
 QY 601 GGGGTCGAGGTGCGGTAAAGCACTAAATCGGAACCTTAAGGAGAGCCCGGATTTAGAGC 660
 Db 5790 GGGGTCGAGGTGCGGTAAAGCACTAAATCGGAACCTTAAGGAGAGCCCGGATTTAGAGC 5731
 QY 661 TTTGACGGGAAAGCCGGGCAACGTTGGCGAAGAAAGGAAAGGAAAGGAGAGCGGG 720
 Db 5730 TTTGACGGGAAAGCCGGGCAACGTTGGCGAAGAAAGGAAAGGAGAGAGCGGG 5671
 QY 721 CGCTAGGCGCTGGCAAGTGTAGCGGTCAAGTGGCGGTAAACCAACACCCCGCGCT 780
 Db 5670 CGCTAGGCGCTGGCAAGTGTAGCGGTCAAGTGGCGGTAAACCAACACCCCGCGCT 5611
 QY 781 TAATGCGCGCTACAGGGCGGCTACTATGTTGTTGACGAGCAGCTATAACGTCGCTTT 840
 Db 5610 TAATGCGCGCTACAGGGCGGCTACTATGTTGTTGACGAGCAGCTATAACGTCGCTTT 5551
 QY 841 CCTCTGTTGAATCAGAGCGGAGCTAAACAGAGGCGCGATTAAAGGATTTTAGACAGGA 900
 Db 5550 CCTCTGTTGAATCAGAGCGGAGCTAAACAGAGGCGCGATTAAAGGATTTTAGACAGGA 5491
 QY 901 ACGGTACGCCAGAAATCTTTGAGAGTGTGTTTATATCAGTCAGGCCACCGAGTAAAGAG 960
 Db 5490 ACGGTACGCCAGAAATCTTTGAGAGTGTGTTTATATCAGTCAGGCCACCGAGTAAAGAG 5431

QY 961 TCTGTCATCAGCAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAGTAATAACATCAC 1020
 Db 5430 TCTGTCATCAGCAATTAACCGTTGTAGCAATACCTCTTTGATTAGTAGTAATAACATCAC 5371
 QY 1021 TTGCTCTAGTAGAAGCACTCAAACTATCGGCTTTGCTGGTAAATATCCAGAACATATTAC 1080
 Db 5370 TTGCTCTAGTAG-AGAACTCAAACTATCGGCTTTGCTGGTAAATATCCAGAACATATTAC 5312
 QY 1081 CGGCAACCAATTCAGCAGGAAACCTCATGGAATATAGCTATGCTTTGACGCTCAATCG 1140
 Db 5311 CGGCAACCAATTCAGCAGGAAACCTCATGGAATATAGCTATGCTTTGACGCTCAATCG 5252
 QY 1141 TCTGAAATGGATTATTTACATTTGGCAGATTCACCACTCAGCAGCAAGTAATAAAGGGA 1200
 Db 5251 CTAAGATATACCTGGCAGACAGCAATATTTTGAATGGCTATTAGTCTTTAATAAAGGGA 5192
 QY 1201 CATTCGGCCAAACAG 1217
 Db 5191 CATTCGGCCAAACAG 5175

RESULT 12
 AAZ51028/C
 ID AAZ51028 standard; DNA; 7084 BP.
 XX AAZ51028;
 AC
 XX 05-JUN-2000 (first entry)
 DT
 XX Modified filamentous phage.
 DE
 XX Modified filamentous phage;
 KW major coat protein; MCP; ligand-binding heterodimeric antibody; ligand;
 KW ss.
 KW Bacteriophage.
 XX
 PN WO200009715-A1.
 XX
 PD 24-FEB-2000.
 XX
 XX 11-AUG-1999; 99WO-US18207.
 XX
 XX 12-AUG-1998; 98US-0096326.
 PR 24-DEC-1998; 98US-0198839.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Kang AS;
 PI
 XX WPI; 2000-224350/19.
 DR
 XX
 PT
 PT polypeptides -
 XX
 PS Disclosure; Fig 4; 38pp; English.
 XX

CC The present sequence is a modified filamentous phage used for modulation
 CC of polypeptide display on the surface which permits facile manipulation
 CC of the valency of display. The gene encoding the polypeptide is fused
 CC into a synthetic copy of a major coat protein (MCP) which enables
 CC incorporation into the phage during assembly of the filament. Modified
 CC filamentous phage expression vector includes a wild type MCP gene; a
 CC leaky inducible promoter; a synthetic MCP gene; and a directional
 CC cloning site for receiving a nucleotide insert. The vectors can be used
 CC for the expression of polypeptides such as ligand-binding heterodimeric
 CC antibodies. They can be used for identifying ligands and for
 CC characterising antibodies.

Sequence 7084 BP; 1739 A; 1469 C; 1485 G; 2391 T; 0 other;
 Query Match 93.7%; Score 1140.4; DB 21; Length 7084;

Best Local Similarity 99.9%; Pred. No. 2e-206;
 Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 76 GCTGTTTCTGTGTAAATTTCTATCCGCTCACAATTTCCACAACATACAGCCGGAAG 135
 Db 7084 GCTGTTTCTGTGTAAATTTCTATCCGCTCACAATTTCCACAACATACAGCCGGAAG 7025
 QY 136 CATAAAGTCTAAAGCCCTGGGGTGCCTAATGAGTGAGCTAACTCAATTAATTCGCTTGG 195
 Db 7024 CATAAAGTCTAAAGCCCTGGGGTGCCTAATGAGTGAGCTAACTCAATTAATTCGCTTGG 6965
 QY 196 CTCACCTCCCGCTTTCCAGTCGGGAAACCTGCTGCTGCCAGCTGCAATTAATGAATCGGCA 255
 Db 6964 CTCACCTCCCGCTTTCCAGTCGGGAAACCTGCTGCTGCCAGCTGCAATTAATGAATCGGCA 6905
 QY 256 ACGCCGGGGAGAGGGGGTTTGGCTATTGGGCGCCAGGGTGGTGTCTTTTTCACCACTG 315
 Db 6904 ACGCCGGGGAGAGGGGGTTTGGCTATTGGGCGCCAGGGTGGTGTCTTTTTCACCACTG 6845
 QY 316 AGACGGGCAACAGCTGATTCGCCCTTCACCGCTGGCCCTGAGAGAGTTGACGAAGCGGT 375
 Db 6844 AGACGGGCAACAGCTGATTCGCCCTTCACCGCTGGCCCTGAGAGAGTTGACGAAGCGGT 6785
 QY 376 CCACGCTGGTTTCCCGCCAGCAGCGGAAATCCTGTTGATGGTGGTTCGGAATCGGCA 435
 Db 6784 CCACGCTGGTTTCCCGCCAGCAGCGGAAATCCTGTTGATGGTGGTTCGGAATCGGCA 6725
 QY 436 AATCCCTTATAATCAAAAGATAGCCGAGATAGGTTGAGTGTTCACAGTTTGGAA 495
 Db 6724 AATCCCTTATAATCAAAAGATAGCCGAGATAGGTTGAGTGTTCACAGTTTGGAA 6665
 QY 496 CAAGAGTCCACTATTAAAGAACGTGGACTCCAAAGCTCAAGAGCGGAAACCTCTATCA 555
 Db 6664 CAAGAGTCCACTATTAAAGAACGTGGACTCCAAAGCTCAAGAGCGGAAACCTCTATCA 6605
 QY 556 GGGCGATGGCCCACTACGTGAACCATCAACCAATCAAGTTTTCGGGTGAGAGTGGCG 615
 Db 6604 GGGCGATGGCCCACTACGTGAACCATCAACCAATCAAGTTTTCGGGTGAGAGTGGCG 6545
 QY 616 TAAAGCACTTAAATCGAACCTTAAAGGAGAGCCCGCATTTAGAGCTTGACGGGAAAGCC 675
 Db 6544 TAAAGCACTTAAATCGAACCTTAAAGGAGAGCCCGCATTTAGAGCTTGACGGGAAAGCC 6485
 QY 676 GCGCAACGTGGCGAAGGAAAGGAAAGCAAGCAAGCGGCGCTAGGCGCTGCG 735
 Db 6484 GCGCAACGTGGCGAAGGAAAGGAAAGCAAGCAAGCGGCGCTAGGCGCTGCG 6425
 QY 736 AAGTGTAGCGTCAAGCTGCGGTAAACCAACACACCCCGCGCTTAATGCGCGCTACA 795
 Db 6424 AAGTGTAGCGTCAAGCTGCGGTAAACCAACACACCCCGCGCTTAATGCGCGCTACA 6365
 QY 796 GGGCGGTACTATGTTGCTTTGACGAGCAGCTATAACGCTGCTTCCCTGTTGGAAATCAG 855
 Db 6364 GGGCGGTACTATGTTGCTTTGACGAGCAGCTATAACGCTGCTTCCCTGTTGGAAATCAG 6305
 QY 856 AGCGGGAGCTAAACAGGAGCGGATTAAGGATTTTACAGAGAACGCTAGCCAGAAAT 915
 Db 6304 AGCGGGAGCTAAACAGGAGCGGATTAAGGATTTTACAGAGAACGCTAGCCAGAAAT 6245
 QY 916 CTTGAGAAGTCTTTTATAATCAGTGAGCGCCAGCTAAAGAGTCTGTCCATCAGCA 975
 Db 6244 CTTGAGAAGTCTTTTATAATCAGTGAGCGCCAGCTAAAGAGTCTGTCCATCAGCA 6185
 QY 976 AATTAACGTTGTAGCAATACCTTCTTGTATTAGTAATAACATCACTTCCCTGAGTAGAG 1035
 Db 6184 AATTAACGTTGTAGCAATACCTTCTTGTATTAGTAATAACATCACTTCCCTGAGTAGAG 6125
 QY 1036 AACTCAAACTATCGGCTTCTGCTGTAATATCCAGAACATATTACCGCCAGCAATTCGAA 1095
 Db 6124 AACTCAAACTATCGGCTTCTGCTGTAATATCCAGAACATATTACCGCCAGCAATTCGAA 6065
 QY 1096 CAGGAAACGCTCATGGAATACCTACATTTTTCAGCTCAATGCTGCTGAATGATTAT 1155

Db 6064 CAGGAAAAACGCTCATGGAATACCTACATTTTGACGCTCAATCGTCTGAATGGATTAT 6005
 QY 1156 TTACATTGGCAGATTTCACCAAGTCCACAGCAGGACAGTAATAAAGGACATTTTCGCCAACAG 1215
 Db 6004 TTACATTGGCAGATTTCACCAAGTCCACAGCAGGACAGTAATAAAGGACATTTTCGCCAACAG 5945
 QY 1216 AG 1217
 Db 5944 AG 5943

RESULT 13
 AAV03651/c
 ID AAV03651 standard; DNA; 7317 BP.

XX AAV03651;
 XX AC
 XX DT 02-APR-1998 (first entry)
 XX DE M13-based vector M13IX11.

XX Vector construction; T-cell receptor; antibody production; diagnosis;
 KW heteromeric receptor; immunoglobulin superfamily; therapy; circular;
 KW M13-based vector; ds.

XX Synthetic.

XX US5698426-A.

XX 16-DEC-1997.

XX 05-JUN-1995; 95US-0464136.

XX 27-SEP-1991; 91US-0767136.

XX 28-SEP-1990; 90US-0590219.

XX 13-SEP-1993; 93US-0120648.

XX 01-DEC-1994; 94US-0349131.

XX 05-JUN-1995; 95US-0464136.

XX (IXSY-) IXSYS INC.

XX Huse WD;

XX WPT: 1998-051489/05.

XX Construction of heteromeric receptor libraries - by combining
 PT vectors encoding different immunoglobulin fragments

XX Example 1; Column 27-34; 57pp; English.

XX This sequence represents a M13-based vector constructed using the method
 CC of the invention, and the primers shown in AAV03629-V03649. The method
 CC of the invention is for constructing a diverse population of vectors
 CC capable of expressing diverse populations of first and second
 CC polypeptides which form a diverse population of heteromeric receptors of
 CC the immunoglobulin superfamily, and comprises: (a) operationally linking
 CC to a first vector a first population of diverse DNA sequences within a
 CC first gene family encoding a diverse population of first polypeptides of
 CC the heteromeric receptor of the immunoglobulin superfamily, the first
 CC vector having two pairs of restriction sites symmetrically oriented about
 CC a cloning site; (b) operationally linking to a second vector a second
 CC population of diverse DNA sequences within a second gene family encoding
 CC a diverse population of second polypeptides of the heteromeric receptor
 CC of the immunoglobulin superfamily, the second vector having two pairs of
 CC restriction sites symmetrically oriented about a cloning site in an
 CC identical orientation to that of the first vector, where polypeptides
 CC encoded by the first and second gene families are known to form
 CC heteromeric receptors of the immunoglobulin superfamily; and (c)
 CC combining the vector sequences produced by steps (a) and (b) under
 CC conditions which allow only the operational combinations of the vector
 CC sequences containing the first and second populations of diverse DNA
 CC sequences. The method is used to produce diverse populations of
 CC antibodies or T-cell receptors for diagnostic or therapeutic purposes.

XX Sequence 7317 BP; 1787 A; 1555 C; 1547 G; 2428 T; 0 other;
 SQ Query Match 93.0%; Score 1131.4; DB 19; Length 7317;
 Best Local Similarity 99.5%; Pred. No. 1e-204;
 Matches 1135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 77 CTGTTTCTCTGTGAAATTTGTTATCCGCTCACAATTTCCACACAACATACGAGCGGAAGC 136
 Db 6214 CTCTTTGGCGTGTGAAATTTGTTATCCGCTCACAATTTCCACACAACATACGAGCGGAAGC 6155
 QY 137 ATAAAGTCTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTCGGTTGCC 196
 Db 6154 ATAAAGTCTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTCGGTTGCC 6095
 QY 197 TCACGTGCCCGCTTCCAGTCGGGAAACCTGTCTGCCACCTGCATTAATTAATTCGGCCAA 256
 Db 6094 TCACGTGCCCGCTTCCAGTCGGGAAACCTGTCTGCCACCTGCATTAATTAATTCGGCCAA 6035
 QY 257 CGCGGGGAGAGCGGCTTTCGCTATTTGGCGCCAGGCTGGTTTCTTTTCCACCACTGTA 316
 Db 6034 CGCGGGGAGAGCGGCTTTCGCTATTTGGCGCCAGGCTGGTTTCTTTTCCACCACTGTA 5975
 QY 317 GACGGGCAACAGCTGATTTGCCCTTTCACCGCCTGGCCCTGAGAGAGTTGCAGCAAGGGTC 376
 Db 5974 GACGGGCAACAGCTGATTTGCCCTTTCACCGCCTGGCCCTGAGAGAGTTGCAGCAAGGGTC 5915
 QY 377 CACGCTGGTTTCCCGCAGCAGGGGAAAATCTGTTTGTATGTTGGTTCGGAATTCGGCAAA 436
 Db 5914 CACGCTGGTTTCCCGCAGCAGGGGAAAATCTGTTTGTATGTTGGTTCGGAATTCGGCAAA 5855
 QY 437 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTCTGTGTTCCAGTTTGGAAAC 496
 Db 5854 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTCTGTGTTCCAGTTTGGAAAC 5795
 QY 497 AAGAGTCCACTATTAAGAAACAGTGGACTCCACGTCAAGGGGGGAAAACCGTCTATCAG 556
 Db 5794 AAGAGTCCACTATTAAGAAACAGTGGACTCCACGTCAAGGGGGGAAAACCGTCTATCAG 5735
 QY 557 GCGGATGGCCCACTACGTGNAACCATCACCACCAATCAAGTTTTCGTTGGGTTCGAGTGCCT 616
 Db 5734 GCGGATGGCCCACTACGTGNAACCATCACCACCAATCAAGTTTTCGTTGGGTTCGAGTGCCT 5675
 QY 617 AAGACACTAAATCGGAACCCCTAAAGGAGAGCCCGCGATTTAGAGCTTGACGGGGAAGCCG 676
 Db 5674 AAGACACTAAATCGGAACCCCTAAAGGAGAGCCCGCGATTTAGAGCTTGACGGGGAAGCCG 5615
 QY 677 GCGAAGTGGCGAGAAAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 736
 Db 5614 GCGAAGTGGCGAGAAAGGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5555
 QY 737 AGTGTACGGCTACGCTGCGCGTAACCCACACACCCCGCGCTTAATTCGCCCGCTACAG 796
 Db 5554 AGTGTACGGCTACGCTGCGCGTAACCCACACACCCCGCGCTTAATTCGCCCGCTACAG 5495
 QY 797 GCGCGCTACTATGTTGCTTTTGACGAGCAGCTATTAACGTGCTTTCCTGCTTGGTAATCAGA 856
 Db 5494 GCGCGCTACTATGTTGCTTTTGACGAGCAGCTATTAACGTGCTTTCCTGCTTGGTAATCAGA 5435
 QY 857 GCGGGAGCTAAACAGAGGCGGATTAAGGGATTTTACAGAGGAGGAGGAGGAGGAGGAGGAG 916
 Db 5434 GCGGGAGCTAAACAGAGGCGGATTAAGGGATTTTACAGAGGAGGAGGAGGAGGAGGAGGAG 5375
 QY 917 TTGAGAGTGTGTTTATAATCAAGTGGCCACCGAGTAAAGAGAGTCTCTCCATCACGAA 976
 Db 5374 TTGAGAGTGTGTTTATAATCAAGTGGCCACCGAGTAAAGAGAGTCTCTCCATCACGAA 5315
 QY 977 ATTAACCGTTGTAGCAATACCTCTTTGATTAGTAAATACATCATCTGCTGAGTGAAGA 1036
 Db 5314 ATTAACCGTTGTAGCAATACCTCTTTGATTAGTAAATACATCATCTGCTGAGTGAAGA 5255
 QY 1037 ACTCAAACTATCGGCCCTTGGTGGTAAATTCACAGAACATATTACCCGCCAGCCATTGCAAC 1096

Db	5254	ACTCAACCTATCGGCCTTGCTGGTAATATCCAGACAATATTTACGGCAGCCATTGCAAC	5195
Qy	1097	AGGAAAAACGCTCATGGAAATACCTACATTTTTCACGCTCAATCTCTGAAATGGATTATT	1156
Db	5194	AGGAAAAACGCTCATGGAAATACCTACATTTTTCACGCTCAATCTCTGAAATGGATTATT	5135
Qy	1157	TACATTGGCGAGATTCCACAGTCACAGCAGCAGTAAATAAAGGGACATTTGGGCCAACAGA	1216
Db	5134	TACATTGGCGAGATTCCACAGTCACAGCAGCAGTAAATAAAGGGACATTTGGGCCAACAGA	5075
Qy	1217	G 1217	
Db	5074	G 5074	

RESULT 14
AAX16953/C
ID AAX16953 standard; DNA; 7317 BP.

New surface expression libraries expressing heteromeric receptors -
 comprising cells containing vectors containing combinations of DNA
 sequences encoding first and second polypeptides
 Example 1; Fig 3A-C; 58pp; English.
 The invention relates to the expression of heteromeric receptor
 proteins, e.g. from an immunoglobulin (Ig) superfamily, in cells
 containing the heteromeric receptor genes on a single plasmid.
 Especially mentioned, the cell may be a bacteriophage, where the receptor
 protein are expressed as fusion proteins with the surface protein gpIII.
 This sequence represents as fusion proteins with the surface protein gpIII
 of the light chain proteins. the plasmid M13X1 which is used for expression
 AAX16938-16952. The methods can be used to generate diverse populations
 of heteromeric receptors which mimic the natural immune system and can be
 used for diagnostic and therapeutic purposes.
 Sequence 7317 BP; 1787 A; 1555 C; 1547 G; 2428 T; 0 other;

QY	77	CTGTTTCTCGTGTGAAATTGTTATTCGCGCTCACAAATCCACACAACTATACGAGCCGGAAGC	136
DB	6214	CTCTTTTGGGGTGTGAAATTGTTATTCGCGCTCACAAATCCACACAACTATACGAGCCGGAAGC	6155
QY	137	ATAAAGTGTAAAGCCCTGGGGTGCCTAATGAGTGAAGCTAACTCACAATTAATTCGGTTCGCGC	196
DB	6154	ATAAAGTGTAAAGCCCTGGGGTGCCTAATGAGTGAAGCTAACTCACAATTAATTCGGTTCGCGC	6095
QY	197	TCAGTGCCTCCCTTTTCAGTTCGGGAACCTGTCTGTCCAGCTGCATTAAATGAATCGGCCAA	256
DB	6094	TCAGTGCCTCCCTTTTCAGTTCGGGAACCTGTCTGTCCAGCTGCATTAAATGAATCGGCCAA	6035
QY	257	CGCGGGGAGAGGGCGTTTTCGCTATTGGCGCCACGGTGGTTTCTTTTTCACCACTGTA	316
DB	6034	CGCGGGGAGAGGGCGTTTTCGCTATTGGCGCCACGGTGGTTTCTTTTTCACCACTGTA	5975
QY	317	GACGGCAACAGCTGATTTGCCCTTTCACCGCTTGCCCTTGAGAGATTGACAGCAAGCGGTC	376
DB	5974	GACGGCAACAGCTGATTTGCCCTTTCACCGCTTGCCCTTGAGAGATTGACAGCAAGCGGTC	5915
QY	377	CACGCTGGTTTTCGCCACGAGCGGGAANAATCTGTGTTGATGGTGGTTCGGAATTCGGCAAA	436
DB	5914	CACGCTGGTTTTCGCCACGAGCGGGAANAATCTGTGTTGATGGTGGTTCGGAATTCGGCAAA	5855
QY	437	ATCCCTTATTAATCAAAAGATAGCCCGAGATAGGGTTGAGTCTCTGCTCCAGTTTTCGAAC	496
DB	5854	ATCCCTTATTAATCAAAAGATAGCCCGAGATAGGGTTGAGTCTCTGCTCCAGTTTTCGAAC	5795
QY	497	AAAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAAGCGGGAANAACCGTCTATCAG	556
DB	5794	AAAGTCCACTATTAAAGAACGTGGACTCCAACGTCAAAAGCGGGAANAACCGTCTATCAG	5735
QY	557	GGCGATGCCACTACTAGTGAACCATCACCCTAAATCAAGTTTTCGGGTTCGAGTTCGCCGT	616
DB	5734	GGCGATGCCACTACTAGTGAACCATCACCCTAAATCAAGTTTTCGGGTTCGAGTTCGCCGT	5675
QY	617	AAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCCGATTAGAGCTTGACGGGGAAGCCG	676
DB	5674	AAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCCGATTAGAGCTTGACGGGGAAGCCG	5615
QY	677	GCGAAGTGGCGAGAAAGGAAGAAAGCAAGGAGCGGGCGCTAGGCGCGCTGGCA	736
DB	5614	GCGAAGTGGCGAGAAAGGAAGAAAGCAAGGAGCGGGCGCTAGGCGCGCTGGCA	5555
QY	737	AGTGTAGCGGTACCGCTCGCGGTAAACCAACACCGCCGCGCTTAATGCGCGCTACAG	796
DB	5554	AGTGTAGCGGTACCGCTCGCGGTAAACCAACACCGCCGCGCTTAATGCGCGCTACAG	5495
QY	797	GGCGGTACTATGTTGCTTTTGACGAGCACGTATAACGTCTTTCCTCGTTTGGAAATCAGA	856
DB	5494	GGCGGTACTATGTTGCTTTTGACGAGCACGTATAACGTCTTTCCTCGTTTGGAAATCAGA	5435
QY	857	GCGGAGGTAACAGGAGCGCGATTAAAGGGATTTTAGACGAACCGGTACGCCGAATC	916
DB	5434	GCGGAGGTAACAGGAGCGCGATTAAAGGGATTTTAGACGAACCGGTACGCCGAATC	5375
QY	917	TTGAGAAGTGTTTTATAATCAGTGAAGCCACCGAGTAAAGAGTCTGTCCATCAGCAAA	976
DB	5374	TTGAGAAGTGTTTTATAATCAGTGAAGCCACCGAGTAAAGAGTCTGTCCATCAGCAAA	5315
QY	977	ATTAACCGCTGTACCAATCTCTTTGATTAGTATAACATCAGTTCGCTGAGTAGAAGA	1036
DB	5314	ATTAACCGCTGTACCAATCTCTTTGATTAGTATAACATCAGTTCGCTGAGTAGAAGA	5255
QY	1037	ACTCAAACTATCGGCCCTTGTGGTAAATATCAGAACAAATATTACCGCCAGCCATTGCAAC	1096
DB	5254	ACTCAAACTATCGGCCCTTGTGGTAAATATCAGAACAAATATTACCGCCAGCCATTGCAAC	5195
QY	1097	AGGAAAAACGCTATGGAAATACCTTACATTTTGAGCTCAATCGTCTGAAATGGATTATT	1156
DB	5194	AGGAAAAACGCTATGGAAATACCTTACATTTTGAGCTCAATCGTCTGAAATGGATTATT	5135
Y	1157	TACATTTGGCAGATTTCACGAGTACACAGCACCAAGTAAATAAAGGGAGACATTCTGGCCAAACAGA	1216

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Db 5134 TACATGGCAGATTACACAGTACACAGCAGTAATAAAGGAGACATCTGGCCACAGA 5075

Qy 1217 G 1217
Db 5074 G 5074

RESULT 15
AAZ91525/C
ID AAZ91525 standard; DNA; 7317 BP.

XX AC AAZ91525;
XX DT 25-MAY-2000 (first entry)

XX Kappa light chain library nucleotide sequence of M13X11.

XX Bacteriophage M13 vector; prokaryotic cell; heteromeric receptor;
KW antibody; immune system; filamentous bacteriophage; cloning;
XX screening; coexpression; ds.

XX Mus sp.
OS Bacteriophage M13.
OS Synthetic.

XX US6027933-A.

XX 22-FEB-2000.

XX 05-JUN-1995; 95US-0470297.

XX 01-DEC-1994; 94US-0349131.

XX 27-SEP-1991; 91US-0767136.

XX 28-SEP-1990; 90US-0590219.

XX 13-SEP-1993; 93US-0120648.

XX (IXSY-) IXSYS INC.

XX Huse WD;

XX WPI; 2000-194835/17.

XX Kit for the preparation of vectors for the coexpression of two or more
XX DNA sequences encoding proteins that form heteromeric receptors -
XX Example 1; Fig 3; 58pp; English.

XX The present invention describes a kit (I) for the preparation of vectors
XX for the coexpression of two or more DNA sequences encoding polypeptides
XX comprising two vectors which operatively combine through two pairs of
XX restriction sites to form a single vector. The kit is useful for the
XX preparation of vectors for the coexpression of two or more DNA sequences
XX encoding polypeptides which form heteromeric receptors. The kit simply
XX and efficiently generates a large repertoire of diverse combinations of
XX heteromeric receptors. Only proper combinations of vector portions are
XX randomly brought together for the coexpression of different DNA
XX sequences without loss of population size or diversity. AAZ91524 to
XX AAZ91528 represent bacteriophage M13 vector nucleotide sequences
XX constructed in the exemplification of the present invention. AAZ91529 to
XX AAZ91599 represent oligonucleotides used in the construction of vectors
XX in the exemplification of the present invention.

XX Sequence 7317 BP; 1787 A; 1555 C; 1547 G; 2428 T; 0 other;

Query Match 93.0%; Score 1131.4; DB 21; Length 7317;
Best Local Similarity 99.5%; Pred. No. 1e-204;
Matches 1135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 77 CTGTTTCCCTGTGTAATTTGTTATCGCTCACAATTTCCACACATACGAGCGGAAGC 136
Db 6214 CTCCTTGGCGTGTGAATTTGTTATCGCTCACAATTTCCACACATACGAGCGGAAGC 6155

Qy 137 ATAAAGTAAAGCCCTGGGGTGCCTAATGAGTGAGCTAACTACATTAATTTGGTTGGCC 196
Db 6154 ATAAAGTAAAGCCCTGGGGTGCCTAATGAGTGAGCTAACTACATTAATTTGGTTGGCC 6095
Qy 197 TCACTGCCCGCTTTCCAGTCGGGAAACCTGCTCGTCGACGCTGCATTAATGAATCGGCCAA 256
Db 6094 TCACTGCCCGCTTTCCAGTCGGGAAACCTGCTCGTCGACGCTGCATTAATGAATCGGCCAA 6035
Qy 257 CGCGCGGGGAGAGCGGTTTGGCGTATTGGCGCCAGGGTGGTTTCTTTTCCACAGTGA 316
Db 6034 CGCGCGGGGAGAGCGGTTTGGCGTATTGGCGCCAGGGTGGTTTCTTTTCCACAGTGA 5975
Qy 317 GACGGGCAACAGCTGATTGGCCCTTCACCGCTGGCCCTGAGAGAGTTGCAACAGCGGTC 376
Db 5974 GACGGGCAACAGCTGATTGGCCCTTCACCGCTGGCCCTGAGAGAGTTGCAACAGCGGTC 5915
Qy 377 CACGCTGTTTGGCCCGCAGCAGGCGGAAATCTGTTGATGGTGGTCCGAATCGGCAAA 436
Db 5914 CACGCTGTTTGGCCCGCAGCAGGCGGAAATCTGTTGATGGTGGTCCGAATCGGCAAA 5855
Qy 437 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTTGTTTCCAGTTTGGAAAC 496
Db 5854 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTTGTTTCCAGTTTGGAAAC 5795
Qy 497 AAGAGTCCACTATTAAAGAACGTGACCTCAACAGCTCAAGGCGGCAAAACCGTCTATCAG 556
Db 5794 AAGAGTCCACTATTAAAGAACGTGACCTCAACAGCTCAAGGCGGCAAAACCGTCTATCAG 5735
Qy 557 GCGGATGGCCCACTAGCTGAACCATCAACCAATCAAGTTTGGGGTTCGAGGTGCCGT 616
Db 5734 GCGGATGGCCCACTAGCTGAACCATCAACCAATCAAGTTTGGGGTTCGAGGTGCCGT 5675
Qy 617 AAGACACTAAATCGGAACCCCTAAAGGAGCCGCCGATTTAGAGCTTGAGCGGGAAGCCG 676
Db 5674 AAGACACTAAATCGGAACCCCTAAAGGAGCCGCCGATTTAGAGCTTGAGCGGGAAGCCG 5615
Qy 677 GCGAAGTGGCGAGAAAGGAAGGAAAGCAAGGAGGCGGCGCTAGGGCGCTGGCA 736
Db 5614 GCGAAGTGGCGAGAAAGGAAGGAAAGCAAGGAGGCGGCGCTAGGGCGCTGGCA 5555
Qy 737 ACTGTAGCGGTACGCTGCGCTAAGCACCACCGCCGCGCTTAATGGCGCGCTACAG 796
Db 5554 ACTGTAGCGGTACGCTGCGCTAAGCACCACCGCCGCGCTTAATGGCGCGCTACAG 5495
Qy 797 GCGCGCTACTATGTTGCTTTGACGAGCAGTATAACGCTGCTTCTCGTTGGAATCAGA 856
Db 5494 GCGCGCTACTATGTTGCTTTGACGAGCAGTATAACGCTGCTTCTCGTTGGAATCAGA 5435
Qy 857 CGGGAGCTAAACAGAGGCGCGATTAAAGGATTTTAGACAGGAAACCGTACGCCAGATC 916
Db 5434 CGGGAGCTAAACAGAGGCGCGATTAAAGGATTTTAGACAGGAAACCGTACGCCAGATC 5375
Qy 917 TTGAGAAGTGTGTTTATAATCAGTGAGGCGCACCGAGTAAAGAGTCTGTCATCAGCAAA 976
Db 5374 TTGAGAAGTGTGTTTATAATCAGTGAGGCGCACCGAGTAAAGAGTCTGTCATCAGCAAA 5315
Qy 977 ATTAACCGTTTACCAATCTCTTTGATTAGTAATACATCACTTGCCTGAGTAGAAGA 1036
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Db 5254 ACTCAAACTATCGGCGCTTGGTGAATATCCAGAACATATATACGCCAGCCATTGGCAAC 5195
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Db 5194 AGGAAAACCGCTCATGGAAATACCTACATTTTGGCGCTCAATTCGCTGAAATGGATTATT 5135
Qy 1157 TACATTTGGCAGATTTCACAGTCCACGACAGTAAATAAAGGAGACATTTCTGCCAACAGA 1216
Db 5134 TACATTTGGCAGATTTCACAGTCCACGACAGTAAATAAAGGAGACATTTCTGCCAACAGA 5075

Thu Aug 1 12:08:39 2002

us-10-014-743-1.rng

Page 16

QY 1217 G 1217
Db 5074 G 5074

Search completed: August 1, 2002, 09:37:26
Job time: 6762 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 07:40:39 : Search time 87.24 Seconds
(without alignments)
3426.593 Million cell updates/sec

Title: US-10-014-743-1
Perfect score: 1217
Sequence: 1 GCCAAGTTCGATCCCTGCA.....GGACATTCGCCACACAG 1217

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues
Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA: *
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2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1217	100.0	1217	1	US-08-726-462B-1
2	1217	100.0	1217	2	US-08-642-330-1
3	1217	100.0	1217	2	US-09-046-203-1
4	1217	100.0	1217	3	US-09-272-104-1
5	1217	100.0	1217	4	US-09-272-097-1
6	1150.8	94.6	7294	1	US-08-440-787A-1
7	1150.8	94.6	7294	1	US-08-440-787A-5
8	1150.8	94.6	7294	4	US-08-367-685-1
9	1150.8	94.6	7294	4	US-08-367-685-5
10	1150.8	94.6	7294	5	PCT-US91-07141-1
11	1150.8	94.6	7294	5	PCT-US91-07141-5
12	1140.4	93.7	7083	4	US-09-198-839-1
13	1131.4	93.0	7317	2	US-08-464-136-2
14	1131.4	93.0	7317	2	US-08-349-131-2
15	1131.4	93.0	7317	3	US-08-470-297A-2
16	1131.4	93.0	7317	5	PCT-US91-07149-2
17	1131.4	93.0	7320	1	US-08-440-787A-2
18	1131.4	93.0	7320	4	US-08-367-685-2
19	1131.4	93.0	7320	5	PCT-US91-07141-2
20	1131.4	93.0	7557	1	US-08-464-136-4
21	1131.4	93.0	7557	2	US-08-349-131-4
22	1131.4	93.0	7557	3	US-08-470-297A-4
23	1131.4	93.0	7557	5	PCT-US91-07149-4
24	1131.4	93.0	8118	1	US-08-464-136-5
25	1131.4	93.0	8118	2	US-08-349-131-5
26	1131.4	93.0	8118	3	US-08-470-297A-5
27	1131.4	93.0	8118	5	PCT-US91-07149-5

C 28	1131	92.9	7394	1	US-08-440-787A-6	Sequence 6, Appli
C 29	1131	92.9	7394	4	US-08-367-685-6	Sequence 6, Appli
C 30	1131	92.9	7394	5	PCT-US91-07141-6	Sequence 6, Appli
C 31	1131	92.9	7409	1	US-08-440-787A-4	Sequence 4, Appli
C 32	1131	92.9	7409	4	US-08-367-685-4	Sequence 4, Appli
C 33	1131	92.9	7409	5	PCT-US91-07141-4	Sequence 4, Appli
C 34	1131	92.9	7445	1	US-08-464-136-1	Sequence 1, Appli
C 35	1131	92.9	7445	1	US-08-440-787A-3	Sequence 3, Appli
C 36	1131	92.9	7445	2	US-08-349-131-1	Sequence 1, Appli
C 37	1131	92.9	7445	4	US-08-470-297A-1	Sequence 1, Appli
C 38	1131	92.9	7445	4	US-08-367-685-3	Sequence 3, Appli
C 39	1131	92.9	7445	5	PCT-US91-07141-3	Sequence 3, Appli
C 40	1131	92.9	7445	5	PCT-US91-07149-1	Sequence 1, Appli
C 41	1131	92.9	7729	1	US-08-464-136-3	Sequence 3, Appli
C 42	1131	92.9	7729	2	US-08-349-131-3	Sequence 3, Appli
C 43	1131	92.9	7729	3	US-08-470-297A-3	Sequence 3, Appli
C 44	1131	92.9	7729	5	PCT-US91-07149-3	Sequence 3, Appli
C 45	846.8	69.6	7652	1	US-07-590-988A-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-726-462B-1
; Sequence 1, Application US/08726462B
; Patent No. 5800996
; GENERAL INFORMATION:
; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED
; TITLE OF INVENTION: FLUORESCENCE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; ADDRESSEE: & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for windows 6.0,
; SOFTWARE: ASCII (DOS) TEXT format
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/726,462B
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; PRIOR APPLICATION DATA: 08/672,196
; APPLICATION NUMBER:
; FILING DATE: June 27, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: PELM4304
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-726-462B-1

Query Match 100.0%; Score 1217; DB 1; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.7e-261;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAAGCTTGCATGCTGACGCTGACCTAGAGATCCCGGGTACCGAGCTCGAATTC 60
DB 1 GCCAAGCTTGCATGCTGACGCTGACCTAGAGATCCCGGGTACCGAGCTCGAATTC 60

QY 61 GTAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTTCCACAAA 120
DB 61 GTAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTTCCACAAA 120

QY 121 CATAGAGCGCGAAGCAATAAGCTGTAAGCCCTGGGGTGCCTAATAGTAGAGTAAGTAC 180
DB 121 CATAGAGCGCGAAGCAATAAGCTGTAAGCCCTGGGGTGCCTAATAGTAGAGTAAGTAC 180

QY 181 ATTAATTCGGTTGGCTCAGCTGCCGCTTCCAGTTCGGGAACCTGTGTCGACGCTGCA 240
DB 181 ATTAATTCGGTTGGCTCAGCTGCCGCTTCCAGTTCGGGAACCTGTGTCGACGCTGCA 240

QY 241 TTAATGAATCGGCACACCGCGGGGAGAGGGGTTTGGCTATTTGGCGCCAGGGTGGTT 300
DB 241 TTAATGAATCGGCACACCGCGGGGAGAGGGGTTTGGCTATTTGGCGCCAGGGTGGTT 300

QY 301 TTCTTTTCCAGCTGAGACGCGCAACAGCTGATTCGCCCTTCCAGCTGCGGCTGAGAGA 360
DB 301 TTCTTTTCCAGCTGAGACGCGCAACAGCTGATTCGCCCTTCCAGCTGCGGCTGAGAGA 360

QY 361 GTTGCAGAACGGGTCCAGCTGTTTGGCCCGCAGCGGAAATCTGTTGATGTTGG 420
DB 361 GTTGCAGAACGGGTCCAGCTGTTTGGCCCGCAGCGGAAATCTGTTGATGTTGG 420

QY 421 TTCCGAATCGGCAAAATCCCTTATAATCAAAAGATAGCCCGGATGAGTGT 480
DB 421 TTCCGAATCGGCAAAATCCCTTATAATCAAAAGATAGCCCGGATGAGTGT 480

QY 481 TGTTCAGTTTGGAAAGAGTCCACTATTAAGAAAGTGGACCTCAACGTCGAAGCGG 540
DB 481 TGTTCAGTTTGGAAAGAGTCCACTATTAAGAAAGTGGACCTCAACGTCGAAGCGG 540

QY 541 AAAAACCGTCTATCAGGCGGATGCCCACTACGTGAACCAATCAAGTTT 600
DB 541 AAAAACCGTCTATCAGGCGGATGCCCACTACGTGAACCAATCAAGTTT 600

QY 601 GGGTCCAGTGGCGTAAAGCACTAAATCGAACCTTAAGGGAGCCCCGATTTAGAGC 660
DB 601 GGGTCCAGTGGCGTAAAGCACTAAATCGAACCTTAAGGGAGCCCCGATTTAGAGC 660

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DB 661 TTGACGGGAAAGCCGCGAAGCTGGCGAGAAAGGAGGAAAGGAGGAGCGG 720

QY 721 CGCTAGGCGCTGCGAAGTGTAGCGGTACGCTGCGGTAACCAACACCCCGCGCT 780
DB 721 CGCTAGGCGCTGCGAAGTGTAGCGGTACGCTGCGGTAACCAACACCCCGCGCT 780

QY 781 TAATGCGCGCTACAGGCGCGTACTATGTTGCTTTCAGAGCAGCTAATAGCTGTT 840
DB 781 TAATGCGCGCTACAGGCGCGTACTATGTTGCTTTCAGAGCAGCTAATAGCTGTT 840

QY 841 CCTCGTTGGAATCAGAGCGGGAGCTAAACAGGAGGCGGATTAAGGAGTTTACAGAGA 900
DB 841 CCTCGTTGGAATCAGAGCGGGAGCTAAACAGGAGGCGGATTAAGGAGTTTACAGAGA 900

QY 901 ACGGTACGCGAGAACTCTGAGAGTGTGTTTATTAATCAGTGAGGCGCAGGTAAGAG 960
DB 901 ACGGTACGCGAGAACTCTGAGAGTGTGTTTATTAATCAGTGAGGCGCAGGTAAGAG 960

QY 961 TCTGTCCATCAGGCAAAATTAACGTTGTAGCAATCTCTTTCATTAGTAATTAACATCAC 1020
DB 961 TCTGTCCATCAGGCAAAATTAACGTTGTAGCAATCTCTTTCATTAGTAATTAACATCAC 1020

QY 1021 TTGCGCTGAGTAGAAGAACTCAAACTATCGCGCTTGTGTTGTAATATCCAGAAATATTAC 1080

DB 1021 TTGCGCTGAGTAGAAGAACTCAAACTATCGCGCTTGTGTTGTAATATCCAGAAATATTAC 1080

QY 1081 CGCCAGCCATTGCAACAGGAAAAACGCTCATGGAATACCTTACATTTTGACGCTCAATCG 1140

DB 1081 CGCCAGCCATTGCAACAGGAAAAACGCTCATGGAATACCTTACATTTTGACGCTCAATCG 1140

QY 1141 TCTGAATGATTTATTTACATTTGCAGATTCACCAAGTCACAGCAGTAAATAAAGGGA 1200

DB 1141 TCTGAATGATTTATTTACATTTGCAGATTCACCAAGTCACAGCAGTAAATAAAGGGA 1200

QY 1201 CATTTGCGCAACAGAG 1217

DB 1201 CATTTGCGCAACAGAG 1217

RESULT 2
US-08-642-330-1
; Sequence 1, Application US/08642330
; Patent No. 5863727
; GENERAL INFORMATION:
; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
; APPLICANT: Division
; TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED
; TITLE OF INVENTION: FLUORESCENCE
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Haynes & Davis
; STREET: 2180 Sand Hill Road, Suite 310
; CITY: Menlo Park
; STATE: California
; COUNTRY: USA
; ZIP: 94025-6935
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for Windows 6.0.
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,330
; FILING DATE:
; CLASSIFICATION: 436
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: PELM4303
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 233-0188
; TELEFAX: (415) 233-1129
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-642-330-1

Query Match 100.0%; Score 1217; DB 2; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.7e-261;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAAGCTTGCATGCTGACGCTGACCTAGAGATCCCGGGTACCGAGCTCGAATTC 60

DB 1 GCCAAGCTTGCATGCTGACGCTGACCTAGAGATCCCGGGTACCGAGCTCGAATTC 60

QY 61 GTAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTTCCACAAA 120

DB 61 GTAATCATGGTCATAGCTGTTTCTGTGTGAAATTTGTTATCCGCTCACAATTTCCACAAA 120

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121 CATACAGCCGGAAGCATAAAGTGTAAAGCCCTGGGGTGCTATGAGTGAGCTAACTCAC 180
181 ATTAATTCGGTTCGGCTCACTCCCGCTTTCAGTCGGGAAACCTCTGTCGCCAGCTGCA 240
181 ATTAATTCGGTTCGGCTCACTCCCGCTTTCAGTCGGGAAACCTCTGTCGCCAGCTGCA 240
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301 TTTCTTTTCCAGCTGAGAGCGGCAACAGCTGATGTCCTTCACCGCTGCGCTGAGAGA 360
301 TTTCTTTTCCAGCTGAGAGCGGCAACAGCTGATGTCCTTCACCGCTGCGCTGAGAGA 360
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361 GTTTCAGCAAGCGCTCAGCTGTTTTCGCCAGAGCGGAAATCTGTTGATGGTG 420
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541 AAAACCGCTATCAGGGCGATGCCACTACGTGAACCATCACCCCAATCAAGTTTTT 600
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661 TTGACGGGAAAGCCGCGAGCTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
661 TTGACGGGAAAGCCGCGAGCTGGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 720
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721 CGTATGGGCGCTGCAAGTGTAGGGTACGCTGCGGTACACACACACCGCGCGCT 780
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781 TAATGCGCGCTGCAAGTGTAGGGTACGCTGCGGTACACACACACCGCGCGCT 840
841 CCTGTTGGATCAGAGCGGAGCTAAACAGAGGCGGATTAAGGGGATTTAGACAGGA 900
841 CCTGTTGGATCAGAGCGGAGCTAAACAGAGGCGGATTAAGGGGATTTAGACAGGA 900
901 ACGTACGCCAGAACTCTTGAAGTGTATTAATAGTGAAGCCCGGAGTAAAGAG 960
901 ACGTACGCCAGAACTCTTGAAGTGTATTAATAGTGAAGCCCGGAGTAAAGAG 960
961 TCTGTCCATCAGCAAAATTAACCGTTGAGCAATCTTCTTGTATGATTAATACATCAC 1020
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1021 TTGCTGAGTGAAGAACTCAAACTATCGGCTTCTGCTGATATATCCAGAAATATTAC 1080
1081 CGCCAGCCATTGCAACAGAGAAAGCGCTCATGGAATACCTACATTTTGAACGCTCAATCG 1140
1081 CGCCAGCCATTGCAACAGAGAAAGCGCTCATGGAATACCTACATTTTGAACGCTCAATCG 1140
1141 TCTGAATGGATTATTATGAGTGGAGATTACAGTCCAGGAGGAGGAGGAGGAGGAGGAG 1200
1141 TCTGAATGGATTATTATGAGTGGAGATTACAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200

1201 CATTCTGCCCAACAGAG 1217
1201 CATTCTGCCCAACAGAG 1217
RESULT 3
US-09-046-203-1
Sequence 1, Application US/09046203
Patent No. 5945526
GENERAL INFORMATION:
APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
APPLICANT: Division
TITLE OF INVENTION: ENERGY TRANSFER DYES WITH ENHANCED
TITLE OF INVENTION: FLUORESCENCE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
STREET: 650 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1050
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
SOFTWARE: Wordperfect for windows 6.0,
SOFTWARE: ASCII (DOS) TEXT format
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,203
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/642,330
FILING DATE: May 3, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/672,196
FILING DATE: June 27, 1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/726,462
FILING DATE: October 4, 1996
ATTORNEY/AGENT INFORMATION:
NAME: David J. Weitz
REGISTRATION NUMBER: 38,362
REFERENCE/DOCKET NUMBER: 16842-746
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 493-9300
TELEFAX: (415) 493-6811
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1217 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-046-203-1

Query Match 100.0%; Score 1217; DB 2; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.7e-261;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GCCAAGCTTCATGCTGCAGGTCGACTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60
DB 1 GCCAAGCTTCATGCTGCAGGTCGACTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60
QY 61 GTAATCATGCTCATAGCTGTTTCTCTGTGTAATTTGTTATCCGCTCACAATTCACACAA 120
DB 61 GTAATCATGCTCATAGCTGTTTCTCTGTGTAATTTGTTATCCGCTCACAATTCACACAA 120
QY 121 CATACGAGCCGGAAGCATAAAGTGTAAAGCCCTGGGGTGCTATGAGTGAGCTAACTCAC 180
DB 121 CATACGAGCCGGAAGCATAAAGTGTAAAGCCCTGGGGTGCTATGAGTGAGCTAACTCAC 180

Qy	181	ATTAAATCGGTTGGCGTCACTGCGCCGCTTTCCAGTCGGGAAACCTGTGCTGCCAGCTGCA	241
Db	181	ATTAAATCGGTTGGCGTCACTGCGCCGCTTTCCAGTCGGGAAACCTGTGCTGCCAGCTGCA	241
Qy	241	TTAATGAATCGGCCAAACGCGGGGAGACGGCGTTTCCGTATTGCGGGCCACGGGTGTTT	300
Db	241	TTAATGAATCGGCCAAACGCGGGGAGACGGCGTTTCCGTATTGCGGGCCACGGGTGTTT	300
Qy	301	TTCTTTTACACAGTGAGACGGGCAACAGCTGATTGCGCTTTCACCGCTGCGCCCTGAGAGA	360
Db	301	TTCTTTTACACAGTGAGACGGGCAACAGCTGATTGCGCTTTCACCGCTGCGCCCTGAGAGA	360
Qy	361	GTTGCGCAAGCGGTCCACGCTGGTTTGGCCCGCAGCAGGCGAAATCCTGTTTGATGGTGG	420
Db	361	GTTGCGCAAGCGGTCCACGCTGGTTTGGCCCGCAGCAGGCGAAATCCTGTTTGATGGTGG	420
Qy	421	TTCCGAAATCGGCAAAATCCCTTATAATCAAAAGAATAGCCCGAGATAGGTTTCAGTGT	480
Db	421	TTCCGAAATCGGCAAAATCCCTTATAATCAAAAGAATAGCCCGAGATAGGTTTCAGTGT	480
Qy	481	TGTTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAAGCTCAAAAGCGG	540
Db	481	TGTTTCCAGTTTGGAAACAAGAGTCCACTATTAAAGAACGTGGACTCCAAGCTCAAAAGCGG	540
Qy	541	AAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTT	600
Db	541	AAAAACCGTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTT	600
Qy	601	GGGTCGAGTGCCTTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCCGATTATAGAGC	660
Db	601	GGGTCGAGTGCCTTAAAGCACTAAATCGGAACCTTAAAGGAGCGCCCGATTATAGAGC	660
Qy	661	TTGACGGGGAAGCCGCGNACGTGCGGAGAAAGGAAGGGAAGAAAGGAGCGG	720
Db	661	TTGACGGGGAAGCCGCGNACGTGCGGAGAAAGGAAGGGAAGAAAGGAGCGG	720
Qy	721	CGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAAACCACACACCCCGCGCT	780
Db	721	CGCTAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGCGTAAACCACACACCCCGCGCT	780
Qy	781	TAAATCGCGCTACAGGGCGGTACTATGTTGCTTTGACGAGCAGTATAACGTGCTTT	840
Db	781	TAAATCGCGCTACAGGGCGGTACTATGTTGCTTTGACGAGCAGTATAACGTGCTTT	840
Qy	841	CCTCGTTGAAATCAGACGGGAGCTAAACAGGAGCCCATTAAGGGATTTTACACAGGA	900
Db	841	CCTCGTTGAAATCAGACGGGAGCTAAACAGGAGCCCATTAAGGGATTTTACACAGGA	900
Qy	901	ACGGTACGCCAGATCTTGAGAAGTCTTTTATACTAGTGAGGCCACCGAGTAAAAGAG	960
Db	901	ACGGTACGCCAGATCTTGAGAAGTCTTTTATACTAGTGAGGCCACCGAGTAAAAGAG	960
Qy	961	TCGTGTCATCAGCAGAAATTAACCGTTGTAGCAATACTTCTTTGATTAGTATAACATCAC	1020
Db	961	TCGTGTCATCAGCAGAAATTAACCGTTGTAGCAATACTTCTTTGATTAGTATAACATCAC	1020
Qy	1021	TTGCCGTAGTAGAAGAACTCAAACCTATCGCGCTTGCTGTTATATCAGAACATATTAC	1080
Db	1021	TTGCCGTAGTAGAAGAACTCAAACCTATCGCGCTTGCTGTTATATCAGAACATATTAC	1080
Qy	1081	CGCCAGCCATTGCCACAGGAAACAGCTCATGGAAATACCTTACATTTTGACGCTCAATCG	1140
Db	1081	CGCCAGCCATTGCCACAGGAAACAGCTCATGGAAATACCTTACATTTTGACGCTCAATCG	1140
Qy	1141	TCTGAAATCGATTATTATACATTGGCAGATTCACCGAGTCACAGCACCAGTAATAAAGGGA	1200
Db	1141	TCTGAAATCGATTATTATACATTGGCAGATTCACCGAGTCACAGCACCAGTAATAAAGGGA	1200
Qy	1201	CATTCTGGCCAACAGAG	1217
Db	1201	CATTCTGGCCAACAGAG	1217

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RESULT      4
US-09-272-104-1
; Sequence 1, Application US/09272104
; Patent No. 6145434
; GENERAL INFORMATION:
; APPLICANT: Perkin-Elmer Corporation, Applied Biosystems
; APPLICANT: Division
; TITLE OF INVENTION: METHOD FOR DETECTING
; TITLE OF INVENTION: OLIGONUCLEOTIDES USING ENERGY TRANSFER DYES WITH LONG STOK
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; ADDRESSEE: & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Wordperfect for windows 6.0,
; SOFTWARE: ASCII (DOS) TEXT format
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,104
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/726,462
; FILING DATE: October 4, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/046,203
; FILING DATE: March 23, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: 16842-755
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 493-9300
; TELEFAX: (415) 493-6811
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-272-104-1

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Db 181 ATTAATTCGCTGGCTCACTGCCCGCTTCCAGTCGGGAACCTGCTGTCACAGCTGCA 240
QY 241 TTAATGAATCGGCAACGCGGGGAGAGGGGTTTTCGCTATTTGGGCGCCAGGGTGGTTT 300
Db 241 TTAATGAATCGGCAACGCGGGGAGAGGGGTTTTCGCTATTTGGGCGCCAGGGTGGTTT 300
QY 301 TTCTTTTACAGTGAAGAGGGAACAGCTGATTTGCCCTTCCAGCTGCGCCCTGAGAGA 360
Db 301 TTCTTTTACAGTGAAGAGGGAACAGCTGATTTGCCCTTCCAGCTGCGCCCTGAGAGA 360
QY 361 GTTCACGAAGCGCTGACAGCTGTTTGGCCGACGAGCGAAATCTCTGTTGATGGTG 420
Db 361 GTTCACGAAGCGCTGACAGCTGTTTGGCCGACGAGCGAAATCTCTGTTGATGGTG 420
QY 421 TTCCGAATCGGCAAAATCCCTTATAATCAAAAGATAGCCCGAGATAGGGTTGAGTGT 480
Db 421 TTCCGAATCGGCAAAATCCCTTATAATCAAAAGATAGCCCGAGATAGGGTTGAGTGT 480
QY 481 TGTTCAGTTTGGAAAGAGTCCACTATTAAAGACGTGACCTCCACAGTCAAGGGCG 540
Db 481 TGTTCAGTTTGGAAAGAGTCCACTATTAAAGACGTGACCTCCACAGTCAAGGGCG 540
QY 541 AAAACCGTCTATCAGGCGGATGCCACTACGTGAACCATCACCAATCAAGTTTTT 600
Db 541 AAAACCGTCTATCAGGCGGATGCCACTACGTGAACCATCACCAATCAAGTTTTT 600
QY 601 GGGTTCGAGTGCCTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGGATTTAGAGC 660
Db 601 GGGTTCGAGTGCCTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGGATTTAGAGC 660
QY 661 TTGACGGGGAAGCGCGGAACTGCGGAGAGAAAGGAGGAGAAAGGAGGAGCGGG 720
Db 661 TTGACGGGGAAGCGCGGAACTGCGGAGAGAAAGGAGGAGAAAGGAGGAGCGGG 720
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Db 721 CGCTAGGCGCTGCAAGTGTAGGGTCACTGCTGCGCTTAACACACACCGCGCGCT 780
QY 781 TAATCGCGCTACAGGCGCGCTACTATGTTGCTTTCAGGAGCAGCTATACGTCGTT 840
Db 781 TAATCGCGCTACAGGCGCGCTACTATGTTGCTTTCAGGAGCAGCTATACGTCGTT 840
QY 841 CCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGGATTTAGACAGGA 900
Db 841 CCTGTTGGAATCAGAGCGGAGCTAAACAGGAGCGGATTAAGGGATTTAGACAGGA 900
QY 901 ACGGTACGCCAGAACTCTTGAAGTGTATTAATCAAGTGAAGGCGGATTAAGAGAG 960
Db 901 ACGGTACGCCAGAACTCTTGAAGTGTATTAATCAAGTGAAGGCGGATTAAGAGAG 960
QY 961 TCTGTCATACGCAAAATTAACCGTTGAGCAATCTCTTTGATTAGTAATACATCAC 1020
Db 961 TCTGTCATACGCAAAATTAACCGTTGAGCAATCTCTTTGATTAGTAATACATCAC 1020
QY 1021 TTGCTGAGTGAAGAACTCAACTATCGGCCCTTCTGCTATATCCAGAAATATTAC 1080
Db 1021 TTGCTGAGTGAAGAACTCAACTATCGGCCCTTCTGCTATATCCAGAAATATTAC 1080
QY 1081 CGCCAGGCGATTAACAGGAAAGCGCTCATGGAATACCTATTTTTCAGCTCAATCG 1140
Db 1081 CGCCAGGCGATTAACAGGAAAGCGCTCATGGAATACCTATTTTTCAGCTCAATCG 1140
QY 1141 TCTGAATGGATTAATTTACATTTGGAGATTTACAGTACAGGAGCAAGTAAGAGGA 1200
Db 1141 TCTGAATGGATTAATTTACATTTGGAGATTTACAGTACAGGAGCAAGTAAGAGGA 1200
QY 1201 CATTCCTGCGCAACAGAG 1217
Db 1201 CATTCCTGCGCAACAGAG 1217

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RESULT 5
US-09-272-097-1
; Sequence 1, Application US/09272097
; Patent No. 6335440
; GENERAL INFORMATION:
; APPLICANT: PE Corporation (NY)
; TITLE OF INVENTION: METHOD FOR DETECTING OLIGONUCLEOTIDES USING
; ENERGY TRANSFER DYES WITH LONG STROKE SHIFT
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David J. Weitz, Wilson Sonsini Goodrich
; & Rosati
; STREET: 650 Page Mill Road
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1050
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; OPERATING SYSTEM: Microsoft Windows 3.1/DOS 5.0
; SOFTWARE: Word 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/272,097
; FILING DATE: 18-Mar-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/642,330
; FILING DATE: May 3, 1996
; APPLICATION NUMBER: 08/672,196
; FILING DATE: June 27, 1996
; APPLICATION NUMBER: 08/728,462
; FILING DATE: October 4, 1996
; APPLICATION NUMBER: 09/046,203
; FILING DATE: March 23, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: David J. Weitz
; REGISTRATION NUMBER: 38,362
; REFERENCE/DOCKET NUMBER: 16842-755
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 493-9300
; TELEFAX: (650) 493-6811
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1217 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-272-097-1

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Query Match 100.0%; Score 1217; DB 4; Length 1217;
Best Local Similarity 100.0%; Pred. No. 1.7e-261;
Matches 1217; Conservative 0; Mismatches 0; Indels 0; Gaps 0:
QY 1 GCCAAGCTTGCATGCTGCAGTGCAGTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60
Db 1 GCCAAGCTTGCATGCTGCAGTGCAGTCTAGAGGATCCCGGGTACCGAGCTCGAATTC 60
QY 61 GTAATCATGTCATAGCTGTTTCTGTTGTAATTTGTTATCCGCTCACAATTCACACAA 120
Db 61 GTAATCATGTCATAGCTGTTTCTGTTGTAATTTGTTATCCGCTCACAATTCACACAA 120
QY 121 CATACGAGCGGAGCAATAAGTGAAGGCTGGGGTGCCTTAATGAGTGAAGTCACTAC 180
Db 121 CATACGAGCGGAGCAATAAGTGAAGGCTGGGGTGCCTTAATGAGTGAAGTCACTAC 180
QY 181 ATTAATTCGCTGGCTCACTGCGCCGCTTCCAGTCGGGAACCTGCTGTCACAGCTGCA 240
Db 181 ATTAATTCGCTGGCTCACTGCGCCGCTTCCAGTCGGGAACCTGCTGTCACAGCTGCA 240

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Db 241 TTAATGAATCGCCCAACCGCGGGGAGAGCGGTTTCGCTATTGGGGCCAGGCTGTTT 300
QY 301 TTCTTTTCCAGCAGTCCAGCGGCAACAGCTGATTCGCCCTTCACCGCTGCCCTCGACAGA 360
Db 301 TTCTTTTCCAGCAGTCCAGCGGCAACAGCTGATTCGCCCTTCACCGCTGCCCTCGACAGA 360
QY 361 GTTCAGCAAGCGGTCCAGCGTGGTTTGGCCAGCAGCGGAAATCCTGTTGATGGTG 420
Db 361 GTTCAGCAAGCGGTCCAGCGTGGTTTGGCCAGCAGCGGAAATCCTGTTGATGGTG 420
QY 421 TTCCGAATCGSCAAATCCCTTATAATCAAAAGATATACCCGAGATAGGTTGAGTGT 480
Db 421 TTCCGAATCGSCAAATCCCTTATAATCAAAAGATATACCCGAGATAGGTTGAGTGT 480
QY 481 TGTTCAGTTTGGAAACAGAGTCCACTATTAAAGAACCTGAGCTCCCAACGTCAAAGGGCG 540
Db 481 TGTTCAGTTTGGAAACAGAGTCCACTATTAAAGAACCTGAGCTCCCAACGTCAAAGGGCG 540
QY 541 AAAAACCGTCTATCAGGCGGATGGCCACTACGTGAACCATCACCCAAATCAAGTTT 600
Db 541 AAAAACCGTCTATCAGGCGGATGGCCACTACGTGAACCATCACCCAAATCAAGTTT 600
QY 601 GGGTTCGAGTGCCTTAAGCACTAAATCGGAACCCCTAAGGAGCGCCCGGATTTAGAGC 660
Db 601 GGGTTCGAGTGCCTTAAGCACTAAATCGGAACCCCTAAGGAGCGCCCGGATTTAGAGC 660
QY 661 TTGACGGGAAAGCGCGGAAAGAGGAAAGGAAAGGAAAGGAAAGGAAAGGAGCGGG 720
Db 661 TTGACGGGAAAGCGCGGAAAGAGGAAAGGAAAGGAAAGGAAAGGAAAGGAGCGGG 720
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Db 721 CGCTAGGCGGTGCAAGTGTAGCGGTACCGTGCAGCTAACCCACACCGCCCGCGT 780
QY 781 TAATGCGCGGTACAGGCGCGTACTATGTTGCTTTGACGAGCAGCTATAAGTCTTT 840
Db 781 TAATGCGCGGTACAGGCGCGTACTATGTTGCTTTGACGAGCAGCTATAAGTCTTT 840
QY 841 CCTGTTGGAAATCAGAGCGGAGCTAAACAGAGCGCCGATTTAAAGGGATTTTAGACAGGA 900
Db 841 CCTGTTGGAAATCAGAGCGGAGCTAAACAGAGCGCCGATTTAAAGGGATTTTAGACAGGA 900
QY 901 ACGGTACGCGAGATCTTGAGAGTGTGTTTATATACGTAGAGCGCCAGCTAAAGAG 960
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Db 961 TCTGTCCATCAGCAAAATTAACCGTTGTAGCAATATCTTTGATTAGTAATAACATCAC 1020
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Db 1081 CGCAGCATTGCAACAGGAAAGCGTCAAGAAATACCTACATTTGACGCTCAATCG 1140
QY 1141 TCTGAAATGGAATTTTACATTTGAGATTCACGAGTCCACAGCAGTAAATAAGGGA 1200
Db 1141 TCTGAAATGGAATTTTACATTTGAGATTCACGAGTCCACAGCAGTAAATAAGGGA 1200
QY 1201 CATTCGCGCAACAGAG 1217
Db 1201 CATTCGCGCAACAGAG 1217
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RESULT 6

US-08-440-787A-1/C
; Sequence 1, Application US/08440787A
; Patent No. 5770434

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; GENERAL INFORMATION:  
; APPLICANT: Huse, William D.  
; TITLE OF INVENTION: Soluble Peptides Having Constrained,  
; Secondary Conformation in Solution and Method of Making  
; TITLE OF INVENTION: Same.  
; NUMBER OF SEQUENCES: 174  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Campbell & Flores LLP  
; STREET: 4370 La Jolla Village Drive, Suite 700  
; CITY: San Diego  
; STATE: California  
; COUNTRY: USA  
; ZIP: 92122  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/440,787A  
; FILING DATE: 15-MAY-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/978,893  
; FILING DATE: 10-NOV-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Campbell, Cathryn A.  
; REGISTRATION NUMBER: 31,815  
; REFERENCE/DOCKET NUMBER: P-IX 1586  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619) 535-9001  
; TELEFAX: (619) 535-8949  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7294 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: circular  
; US-08-440-787A-1
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Query Match 94.6%; Score 1150.8; DB 1; Length 7294;
Best Local Similarity 99.8%; Pred. No. 1e-246; 2; Indels 0; Gaps 0;
Matches 1152; Conservative 0; Mismatches 2;

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QY 124 ACGAGCGGGAAGCATAAAGTGTAAAGCCTGGGGTGCGCTAATGAGTGAGCTTAACATC 183
Db 6166 ACGAGCGGGAAGCATAAAGTGTAAAGCCTGGGGTGCGCTAATGAGTGAGCTTAACATC 6107
QY 184 AATTGCGTTCGCTCAGTCGCCGCTTCCAGTCGGGAAACCTGTCGTCAGCTGCCATTA 243
Db 6106 AATTGCGTTCGCTCAGTCGCCGCTTCCAGTCGGGAAACCTGTCGTCAGCTGCCATTA 6047
QY 244 ATGAATCGGCAACGCGCGGGAGAGCGGTTTTCGCTATTGGGCGCAGGCTGTTTTC 303
Db 6046 ATGAATCGGCAACGCGCGGGAGAGCGGTTTTCGCTATTGGGCGCAGGCTGTTTTC 5987
QY 304 TTTTCCAGCTGAGACGGGCAACACCTGATTCGCCCTTACCGCTGCGCCCTGAGAGGTT 363
Db 5986 TTTTCCAGCTGAGACGGGCAACACCTGATTCGCCCTTACCGCTGCGCCCTGAGAGGTT 5927
QY 364 GCAGCAAGCGGTCCACGCTGTTTCCCGCAGCAGCGGAAATCCCTCTTTGATGTTGTTTC 423
Db 5926 GCAGCAAGCGGTCCACGCTGTTTCCCGCAGCAGCGGAAATCCCTCTTTGATGTTGTTTC 5867
QY 424 CGAAATCGGCAAAATCCCTTATAATCAAAAGAAATAGCCCGAGATAGGTTGAGTGTGT 483
Db 5866 CGAAATCGGCAAAATCCCTTATAATCAAAAGAAATAGCCCGAGATAGGTTGAGTGTGT 5807
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QY 484 TCCAGTTTGGAAACAGAGTCCCACTATTAAAGAACGTGGACATCCAAAGTCAAAGGCGGAA 543
Db 5806 TCCAGTTTGGAAACAGAGTCCCACTATTAAAGAACGTGGACATCCAAAGTCAAAGGCGGAA 5747
QY 544 AACCGTCTATCAGGCGGATGGCCCACTAGTGAACATCACCACCAATCAAGTTTTTTGG 603
Db 5746 AACCGTCTATCAGGCGGATGGCCCACTAGTGAACATCACCACCAATCAAGTTTTTTGG 5687
QY 604 GTCGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGGATTTAGAGCTTG 663
Db 5686 GTCGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGGATTTAGAGCTTG 5627
QY 664 ACGGGGAAAGCGCGGAGAGTGGCGAGAAAGAAAGGAAAGAAAGGAAAGGAGGCGGCG 723
Db 5626 ACGGGGAAAGCGCGGAGAGTGGCGAGAAAGAAAGGAAAGAAAGGAGGCGGCG 5567
QY 724 TAGGGCGCTGCAAGTGTAGCGGTGACGCTGCGCGTAAACACACACCGCGCGCTTAA 783
Db 5566 TAGGGCGCTGCGCAAGTGTAGCGGTGACGCTGCGCGTAAACACACACCGCGCGCTTAA 5507
QY 784 TCGCGCGCTACAGGCGCGCTACTATGTTGCTTTGACGAGCAGTATACGTGCTTCT 843
Db 5506 TCGCGCGCTACAGGCGCGCTACTATGTTGCTTTGACGAGCAGTATACGTGCTTCT 5447
QY 844 CGTTGGAATCAGAGCGGAGCTAAACAGGAGCGCGATTAAGGGATTTAGACAGGAACG 903
Db 5446 CGTTGGAATCAGAGCGGAGCTAAACAGGAGCGCGATTAAGGGATTTAGACAGGAACG 5387
QY 904 GTACGCCAGATCTTCAGAAAGTCTTTTATATCACTGAGCGCCAGTAAAGAGTCT 963
Db 5386 GTACGCCAGATCTTCAGAAAGTCTTTTATATCACTGAGCGCCAGTAAAGAGTCT 5327
QY 964 GTCCATCAGCGAAATTAACCGTTGTAGCAATCTCTTTGATGATTAATCAATCACTTG 1023
Db 5326 GTCCATCAGCGAAATTAACCGTTGTAGCAATCTCTTTGATGATTAATCAATCACTTG 5267
QY 1024 CTTGAGTAGAGAACTCAACTATCGGCTTGTGTAATATCCAGAACATATACCG 1083
Db 5266 CTTGAGTAGAGAACTCAACTATCGGCTTGTGTAATATCCAGAACATATACCG 5207
QY 1084 CAGCCATTTGCAACAGGAAACGCTCATGGAATACCTATTTGACGCTCAATCGTCT 1143
Db 5206 CAGCCATTTGCAACAGGAAACGCTCATGGAATACCTATTTGACGCTCAATCGTCT 5147
QY 1144 GAAATGATTTATTTACATTTGCGAGATTCACAGTCACAGCACAGTAAATAAGGAGAT 1203
Db 5146 GAAATGATTTATTTACATTTGCGAGATTCACAGTCACAGCACAGTAAATAAGGAGAT 5087
QY 1204 TCTGGCCAAACAGAG 1217
Db 5086 TCTGGCCAAACAGAG 5073

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RESULT 7
US-08-440-787A-5/c
; Sequence 5, Application US/08440787A
; Patent No. 5770434
; GENERAL INFORMATION:
; APPLICANT: Huse, William D.
; TITLE OF INVENTION: Soluble Peptides Having Constrained,
; TITLE OF INVENTION: Secondary Conformation in Solution and Method of Making
; TITLE OF INVENTION: Same.
; NUMBER OF SEQUENCES: 174
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/440,787A
; FILING DATE: 15-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/978,893
; FILING DATE: 10-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1586
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7294 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-440-787A-5

```

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Query Match 94.6%; Score 1150.8; DB 1; Length 7294;
Best Local Similarity 99.8%; Pred. No. 1e-246;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATGTGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCCGCTCACAATTCACACACAT 123
Db 6226 ATCTGTGTGTCATAGCTGTTTCTCTGTGTGAATTTGTTATCCGCTCACAATTCACACACAT 6167
QY 124 ACGAGCCGGAAGCATAAAGTGTAAAGCTTGGGTCGCCTAATGAGTGAGTAACTCACAT 183
Db 6166 ACGAGCCGGAAGCATAAAGTGTAAAGCTTGGGTCGCCTAATGAGTGAGTAACTCACAT 6107
QY 184 AATTGCGTTGCGTCACTGCCCGCTTCCAGTCGGGAAACCTGTGTCGACGCTGATTA 243
Db 6106 AATTGCGTTGCGTCACTGCCCGCTTCCAGTCGGGAAACCTGTGTCGACGCTGATTA 6047
QY 244 ATGAATCGGCAACCGCGGGGAGAGCGGTTTGGTATTGGCGCCAGGCTGTTTTC 303
Db 6046 ATGAATCGGCAACCGCGGGGAGAGCGGTTTGGTATTGGCGCCAGGCTGTTTTC 5987
QY 304 TTTTCCAGTGAGAGCGGCAACAGCTGATTCGCCCTTACCGCTGCGCTTGAGAGAT 363
Db 5986 TTTTCCAGTGAGAGCGGCAACAGCTGATTCGCCCTTACCGCTGCGCTTGAGAGAT 5927
QY 364 GCAGCAAGCGGTCCAGCGTGTGTTGCCCGAGGCGGAAATCCTGTTGATGTTGTTTC 423
Db 5926 GCAGCAAGCGGTCCAGCGTGTGTTGCCCGAGGCGGAAATCCTGTTGATGTTGTTTC 5867
QY 424 CGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGT 483
Db 5866 CGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGT 5807
QY 484 TCCAGTTTGGAAACAGAGTCCCACTATTAAAGAACGTGGACATCCAAAGTCAAAGGCGGAA 543
Db 5806 TCCAGTTTGGAAACAGAGTCCCACTATTAAAGAACGTGGACATCCAAAGTCAAAGGCGGAA 5747
QY 544 AACCGTCTATCAGGCGGATGGCCCACTAGTGAACATCACCACCAATCAAGTTTTTTGG 603
Db 5746 AACCGTCTATCAGGCGGATGGCCCACTAGTGAACATCACCACCAATCAAGTTTTTTGG 5687
QY 604 GTCGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGGATTTAGAGCTTG 663
Db 5686 GTCGAGGTGCGCTAAAGCACTAAATCGGAACCTTAAAGGAGCCCGGATTTAGAGCTTG 5627
QY 664 ACGGGGAAAGCGCGGAGAGTGGCGAGAAAGAAAGGAAAGAAAGGAGGCGGCG 723
Db 5626 ACGGGGAAAGCGCGGAGAGTGGCGAGAAAGAAAGGAAAGAAAGGAGGCGGCG 5567

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Db 5146 GAATGGATTATTACATTGGCAGATTACACAGTCCACAGCAGTAATAAAGGACAT 5087

Qy 1204 TCTGCCAACAGAG 1217

Db 5086 TCTGCCAACAGAG 5073

RESULT 10

PCT-US91-07141-1/c

; Sequence 1, Application PC/TUS9107141

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF

; TITLE OF INVENTION: RANDOMIZED PEPTIDES

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

; STREET: 444 South Flower Street, Suite 2000

; CITY: Los Angeles

; STATE: California

; COUNTRY: United States

; ZIP: 90071

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US91/07141

; FILING DATE: 19910927

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Campbell, Cathryn A

; REGISTRATION NUMBER: 31,815

; REFERENCE/DOCKET NUMBER: P31 9072

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (619) 535-9001

; TELEFAX: (619) 535-8949

; INFORMATION FOR SEQ ID NO: 1:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7294 base pairs

; TYPE: NUCLEIC ACID

; STRANDEDNESS: both

; TOPOLOGY: circular

PCT-US91-07141-1

Query Match 94.6%; Score 1150.8; DB 5; Length 7294;

Best Local Similarity 99.8%; Pred. No. 1e-246;

Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 64 ATCATGGTCATAGCTGTTTCTGTTGAAATTTGTTATCCGCTCACAATCCACACAACAT 123

Db 6226 ATCTGGTCATAGCTGTTTCTGTTGAAATTTGTTATCCGCTCACAATCCACACAACAT 6167

Qy 124 ACAGCGCGGAAGCATAAAGTAAAGCTGGGTGCTTAATGAGTACGCTAATCACTACATT 183

Db 6166 ACAGCGCGGAGCATAAAGTAAAGCTGGGTGCTTAATGAGTACGCTAATCACTACATT 6107

Qy 184 AATTGGGTTGCGCTACTGCGCGCTTTCCAGTCGGGAAACCTGTCGTGCGAGCTGCATTA 243

Db 6106 AATTGGGTTGCGCTACTGCGCGCTTTCCAGTCGGGAAACCTGTCGTGCGAGCTGCATTA 6047

Qy 244 ATCAATCGCCACACGCGCGGGAGAGCGGTTTGGGTATTTGGGCGCGAGGTTTTC 303

Db 6046 ATGAATCGGCCAACGCGCGGGAGAGCGGTTTGGGTATTTGGGCGCGAGGTTTTC 5987

Qy 304 TTTTCCAGTACGAGCGGCAACAGCTGATTGCCCTTACCGCTCGCCCTGAGAGATT 363

Db 5986 TTTTCCAGGAGAGCGGCAACAGCTGATTGCCCTTACCGCTCGCCCTGAGAGATT 5927

Qy 364 GCAGCAAGCGGTCCACGCTGGTTTGGCCCGCAGCAGGAAATCCTGTTTATGTTGTTTC 423

Db 5087 TCTGCCAACAGAG 5073

RESULT 11

PCT-US91-07141-5/c

; Sequence 5, Application PC/TUS9107141

; GENERAL INFORMATION:

; APPLICANT: Huse, William D.

; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF

; TITLE OF INVENTION: RANDOMIZED PEPTIDES

; NUMBER OF SEQUENCES: 61

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark

; STREET: 444 South Flower Street, Suite 2000

; CITY: Los Angeles

; STATE: California

; COUNTRY: United States

```

; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/07141
; FILING DATE: 19910927
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 9072
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7294 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: Both
; TOPOLOGY: circular
; PCT-US91-07141-5

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Query Match 94.68; Score 1150.8; DB 5; Length 7294;
Best Local Similarity 99.98; Pred. No. 1e-246;
Matches 1152; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 64 ATCATGTCATAGCTGTTTCCTGTGTGAATGTTATCCGCTCAAAATTTCCACACAACAT 123
DB 6226 ATCTGTCATAGCTGTTTCCTGTGTGAATGTTATCCGCTCAAAATTTCCACACAACAT 6167

QY 124 ACAGCCGGAGACATAAAGTGTAAAGCCCTGGGGTCCCTAATGAGTGAGCTAACTACAT 183
DB 6166 ACAGCCGGAGACATAAAGTGTAAAGCCCTGGGGTCCCTAATGAGTGAGCTAACTACAT 6107

QY 184 AATTCGCTGTCACGTCACGTCGCTGTTCCAGTCGGGAAACCTGTCGTGCAGCTCATTA 243
DB 6106 AATTCGCTGTCACGTCACGTCGCTGTTCCAGTCGGGAAACCTGTCGTGCAGCTCATTA 6047

QY 244 ATGAATCGCCCAACCGCGGGAGAGGGGTTTGGCTATTGGCCGCCAGGGGTTTTC 303
DB 6046 ATGAATCGCCCAACCGCGGGAGAGGGGTTTGGCTATTGGCCGCCAGGGGTTTTC 5987

QY 304 TTTTCACAGTGAGAGCGGCAACAGCTGATTCGCCCTTCACGCCCTGGCCCTGAGAGATT 363
DB 5986 TTTTCACAGTGAGAGCGGCAACAGCTGATTCGCCCTTCACGCCCTGGCCCTGAGAGATT 5927

QY 364 GCAGCAAGCGTCCACGCTGTTTCCGCCAGCAGCGGAAATCCTGTTGATGGTGGTTC 423
DB 5926 GCAGCAAGCGTCCACGCTGTTTCCGCCAGCAGCGGAAATCCTGTTGATGGTGGTTC 5867

QY 424 CGAAATCGCCAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGT 483
DB 5866 CGAAATCGCCAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGT 5807

QY 484 TCCAGTTGGGAACAAGAGTCCACTATTAAAGACGTGGACTCCAAGCTCAAGGGCGAAA 543
DB 5806 TCCAGTTGGGAACAAGAGTCCACTATTAAAGACGTGGACTCCAAGCTCAAGGGCGAAA 5747

QY 544 AACCGCTATACGGGGGATGGCCCACTACGTGAACCATCACCAAAATCAAGTTTTCGG 603
DB 5746 AACCGCTATACGGGGGATGGCCCACTACGTGAACCATCACCAAAATCAAGTTTTCGG 5687

QY 604 GTCAGGTCGCTTAAAGCACTAAATCGGAACCTAAAGGAGGCCGCCGATTTAGAGCTTG 663
DB 5686 GTCAGGTCGCTTAAAGCACTAAATCGGAACCTAAAGGAGGCCGCCGATTTAGAGCTTG 5627

QY 664 ACAGGGAAGCCGGGAGAGCTGGCGAGAAAGGAGGAGAAAGCGAAGGAGCGGGCCG 723
DB 5626 ACAGGGAAGCCGGGAGAGCTGGCGAGAAAGGAGGAGAAAGCGAAGGAGCGGGCCG 5567

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QY 724 TAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAACCAACACACCCGCGCTTAA 783
DB 5566 TAGGGCGCTGGCAAGTGTAGCGGTACGCTGCGGTAACCAACACACCCGCGCTTAA 5507

QY 784 TCGCGCGCTACAGGGCGGCTACTATGCTTTGACGAGCAGTATAAGCTGCTTTCCT 843
DB 5506 TCGCGCGCTACAGGGCGGCTACTATGCTTTGACGAGCAGTATAAGCTGCTTTCCT 5447

QY 844 CGTTGGAATCAGAGCGGGAGCTAAACAGAGGCGCGATTAAAGGATTTTACAGAGAACG 903
DB 5446 CGTTGGAATCAGAGCGGGAGCTAAACAGAGGCGCGATTAAAGGATTTTACAGAGAACG 5387

QY 904 GTACGCCAGAACTCTTGAGAAAGTCTTTTATATCAATGAGGCGCCAGGTAAGAGCTCT 963
DB 5386 GTACGCCAGAACTCTTGAGAAAGTCTTTTATATCAATGAGGCGCCAGGTAAGAGCTCT 5327

QY 964 GTCCATACGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTAAATCAATCACTTG 1023
DB 5326 GTCCATACGCAAAATTAACCGTTGTAGCAATCTCTTTGATTAGTAAATCAATCACTTG 5267

QY 1024 CCTGAGTAGAAGAACTCAAACTATCGGCTTGTGCTTAATATCCAGAACATATTACCGC 1083
DB 5266 CCTGAGTAGAAGAACTCAAACTATCGGCTTGTGCTTAATATCCAGAACATATTACCGC 5207

QY 1084 CAGCCATTGCAACAGAGGAAACCGCTCATGGAATACCTACATTTTGACGCTCAATCGTCT 1143
DB 5206 CAGCCATTGCAACAGAGGAAACCGCTCATGGAATACCTACATTTTGACGCTCAATCGTCT 5147

QY 1144 GAAATGGATTATTATTCATTTGGCAGATTCCAGCTACAGCAGCAGTAAATCAAGGGACAT 1203
DB 5146 GAAATGGATTATTATTCATTTGGCAGATTCCAGCTACAGCAGCAGTAAATCAAGGGACAT 5087

QY 1204 TCTGGCCCAACAGAG 1217
DB 5086 TCTGGCCCAACAGAG 5073

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RESULT 12
US-09-198-839-1/c
; Sequence 1, Application US/09198839
; Patent No. 6190908
; GENERAL INFORMATION:
; APPLICANT: Kang, Angray S.
; TITLE OF INVENTION: MODULATION OF POLYPEPTIDE DISPLAY ON MODIFIED
; FILE OF INVENTION: FILAMENTOUS PHAGE
; FILE REFERENCE: SCR21115
; CURRENT APPLICATION NUMBER: US/09/198,839
; CURRENT FILING DATE: 1998-12-24
; PRIOR APPLICATION NUMBER: PCT/US99/18207
; PRIOR FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: 60/096,326
; PRIOR FILING DATE: 1998-08-12
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7083
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: a modified
; OTHER INFORMATION: filamentous phage
US-09-198-839-1

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Query Match 93.78; Score 1140.4; DB 4; Length 7083;
Best Local Similarity 99.98; Pred. No. 2e-244;
Matches 1141; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 76 GCTGTTTCCTGTGTGAATTTGTTATCCGCTCACAAATTCACACAAATACGAGCGGAAG 135
DB 7083 GCTGTTTCCTGTGTGAATTTGTTATCCGCTCACAAATTCACACAAATACGAGCGGAAG 7024

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QY	136	CATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTCGGCTTGGC	195
Db	7023	CATAAAGTGTAAAGCCTGGGGTGCCTAATGAGTGAGCTAACTCACATTAATTCGGCTTGGC	6964
QY	196	CTCACTGCCCGCTTTCAGTCGGGAAACCTGCTGCCACGTCGATTTAATGAATCGGCCA	255
Db	6963	CTCACTGCCCGCTTTCAGTCGGGAAACCTGCTGCCACGTCGATTTAATGAATCGGCCA	6904
QY	256	ACGCGCGGGGAGAGCGGTTTGGGTATTTGGGCCGCCAGGGTGGTTTTCTTTTCCACCAAGT	315
Db	6903	ACGCGCGGGGAGAGCGGTTTGGGTATTTGGGCCGCCAGGGTGGTTTTCTTTTCCACCAAGT	6844
QY	316	AGACGGGCACACGCTCATTTGCCCTTCACGCCCTGGGCCCTGAGAGAGTTGCAGCAAGCGGT	375
Db	6843	AGACGGGCACACGCTCATTTGCCCTTCACGCCCTGGGCCCTGAGAGAGTTGCAGCAAGCGGT	6784
QY	376	CCACGCTGGTTTTGCCCCAGCAGCGGAAAATCCCTGTTTGATGGTGGTTCCGAAATCGGCAA	435
Db	6783	CCACGCTGGTTTTGCCCCAGCAGCGGAAAATCCCTGTTTGATGGTGGTTCCGAAATCGGCAA	6724
QY	436	AATCCGTTATAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAA	495
Db	6723	AATCCGTTATAATCAAAAGAAATAGCCCGAGATAGGGTTGAGTGTGTTCCAGTTTGGAA	6664
QY	496	CAAGAGTCCACTATTAAAGAACGTGGACATCCACGTCAAAGGGCGAAACCGCTCATCA	555
Db	6663	CAAGAGTCCACTATTAAAGAACGTGGACATCCACGTCAAAGGGCGAAACCGCTCATCA	6604
QY	556	GGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTGGGGTCGAGGTGCCG	615
Db	6603	GGCGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTGGGGTCGAGGTGCCG	6544
QY	616	TAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAGCC	675
Db	6543	TAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCCGATTTAGAGCTTGACGGGGAAGCC	6484
QY	676	GGCGAACGTGGCGAGAAAGGAAGGAAGCAAGAGCGGGCGCTTAGGGCGCTGGC	735
Db	6483	GGCGAACGTGGCGAGAAAGGAAGGAAGCAAGAGCGGGCGCTTAGGGCGCTGGC	6424
QY	736	AAGTGTAGCGGTACGCTGCGCGTTAACACACACACCGCGCGCTTAAATGCGCGCTGAC	795
Db	6423	AAGTGTAGCGGTACGCTGCGCGTTAACACACACACCGCGCGCTTAAATGCGCGCTGAC	6364
QY	796	GGCGCGTACTATGCTTGTGTTGACGAGCAGCCTATAACGTGCTTTCCTCGTTGGAATCAG	855
Db	6363	GGCGCGTACTATGCTTGTGTTGACGAGCAGCCTATAACGTGCTTTCCTCGTTGGAATCAG	6304
QY	856	ACGCGGAGCTTAACAGAGGCGGATTAAGGGATTTTAGCAGGAACGGTACGCCAGAAT	915
Db	6303	ACGCGGAGCTTAACAGAGGCGGATTAAGGGATTTTAGCAGGAACGGTACGCCAGAAT	6244
QY	916	CTTGAGAAAGTGTTTTATAATCAGTGAGGCCACCGAGTAAAGAGCTCTGCCATCACGCA	975
Db	6243	CTTGAGAAAGTGTTTTATAATCAGTGAGGCCACCGAGTAAAGAGCTCTGCCATCACGCA	6184
QY	976	AATTAAACCGTTGTAGCAATCTCTTTGATTAGTAAATAAACATCACTTGCTCAGTAGAAG	1035
Db	6183	AATTAAACCGTTGTAGCAATCTCTTTGATTAGTAAATAAACATCACTTGCTCAGTAGAAG	6124
QY	1036	AACCTCAACTATCGCCCTTGCTGGTAAATATCCAGAACAAATATTACGCCAGCCATTGCAA	1095
Db	6123	AACCTCAACTATCGCCCTTGCTGGTAAATATCCAGAACAAATATTACGCCAGCCATTGCAA	6064
QY	1096	CAGGAAAACGCTCATGGAATACCTACATTTTGACGCTCAATCGTCTGAAATGGATTAT	1155
Db	6063	CAGGAAAACGCTCATGGAATACCTACATTTTGACGCTCAATCGTCTGAAATGGATTAT	6004
QY	1156	TTACATTTGGCAGATTCACCAAGTCACACGACAGTAAATAAAGGGACATTCCTGGCCAAACAG	1215
Db	6003	TTACATTTGGCAGATTCACCAAGTCACACGACAGTAAATAAAGGGACATTCCTGGCCAAACAG	5944
QY	1216	AG 1217	

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11
Db 5943 AG 5942

RESULT 13
US-08-464-136-2/c
: Sequence 2, Application US/08464136
: Patent No. 5698426
: GENERAL INFORMATION:
: APPLICANT: ROSE, WILLIAM D.
: TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
: TITLE OF INVENTION: HETEROMERIC RECEPTORS
: NUMBER OF SEQUENCES: 75
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: PRETTY, SCHROEDER, BRUEGGEMANN & CLARK
: STREET: 444 SO. FLOWER STREET, SUITE 200
: CITY: LOS ANGELES
: STATE: CALIFORNIA
: COUNTRY: UNITED STATES
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/464.136
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: CAMPBELL, CATHRYN A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P31 8882
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 619-535-9001
: TELEFAX: 619-535-8949
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7317 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: both
: TOPOLOGY: circular
: US-08-464-136-2

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Query Match	93.0%	Score 1131.4	DB 1	Length 7317	
Best Local Similarity	99.5%	Pred. No. 2e+242			
Matches 1135	Conservative 0	Mismatches 6	Indels 0	Gaps 0	
QY	77	CTGTTTCTGTGTCAAATTTGTTATCCGGCTCACAAATTCACACACATACGAGCGCGAAGC	136		
Db	6214	CTCCTTGGCGTGTGAAATTTGTTATCCGGCTCACAAATTCACACACATACGAGCGCGAAGC	6155		
QY	137	ATAAAGTGTAAGAGCTCGGGTGCCCTAATGAGTGAGCTAACTCACATTAATTTGCGTTGGCG	196		
Db	6154	ATAAAGTGTAAGAGCTCGGGTGCCCTAATGAGTGAGCTAACTCACATTAATTTGCGTTGGCG	6095		
QY	197	TCACTGCCCGGTTTCCAGTCGGGAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA	256		
Db	6094	TCACTGCCCGGTTTCCAGTCGGGAACCTGTCGTGCCAGCTGCATTAATGAATCGGCCAA	6035		
QY	257	CGCGCGGGGAGAGCGCGTTTCGCTATTTGGCGCCAGGGTGTTTTCTTTTCACCACTGA	316		
Db	6034	CGCGCGGGGAGAGCGCGTTTCGCTATTTGGCGCCAGGGTGTTTTCTTTTCACCACTGA	5975		
QY	317	GACGGGCAACAGCTGATTTGCCCTTTCACCGCCTCGGCCCTGAGAGAGTTGCAGCAAGCGGTC	376		
Db	5974	GACGGGCAACAGCTGATTTGCCCTTTCACCGCCTCGGCCCTGAGAGAGTTGCAGCAAGCGGTC	5915		
QY	377	CAGCGCTGGTTTGGCCCAAGCAGCGGAAATCTGTTTGATGGTTCGGAATTCGGCAAA	436		
Db	5914	CAGCGCTGGTTTGGCCCAAGCAGCGGAAATCTGTTTGATGGTTCGGAATTCGGCAAA	5855		

QY 437 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTGTTCAGTTTGGAAAC 496
Db 5854 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTGTTCAGTTTGGAAAC 5795
QY 497 AAGAGTCCACTATTAAAGAACGTGGATCCCAACGCTAAAGGGCGAAACCGTCTATCAG 556
Db 5794 AAGAGTCCACTATTAAAGAACGTGGATCCCAACGCTAAAGGGCGAAACCGTCTATCAG 5735
QY 557 GCGGATGGCCCTACTGTTACCATACCCCAATCAAGTTTGTGGGTCCAGTCCGCT 616
Db 5734 GCGGATGGCCCTACTGTTACCATACCCCAATCAAGTTTGTGGGTCCAGTCCGCT 5675
QY 617 AAAGCACTAAATCGAACCCTTAAAGGAGCGCCCGATTTAGAGCTTGACGGGAAAGCGG 676
Db 5674 AAAGCACTAAATCGAACCCTTAAAGGAGCGCCCGATTTAGAGCTTGACGGGAAAGCGG 5615
QY 677 GCGAAGTGGCGGAGAAAGGAGGAGAAAGCGAAAGAGGAGCGGGCTAGGGCGTGGCA 736
Db 5614 GCGAAGTGGCGGAGAAAGGAGGAGAAAGCGAAAGAGGAGCGGGCTAGGGCGTGGCA 5555
QY 737 AGTGTAGCGTTCAGCTGCGGCTAACCCACACACCGCGCTTAATCGCGCTACAG 796
Db 5554 AGTGTAGCGTTCAGCTGCGGCTAACCCACACACCGCGCTTAATCGCGCTACAG 5495
QY 797 GCGCGTACTATGTTGCTTTGAGGAGCAGCTATAACGCTGCTTCTCGTTGGATCAGA 856
Db 5494 GCGCGTACTATGTTGCTTTGAGGAGCAGCTATAACGCTGCTTCTCGTTGGATCAGA 5435
QY 857 GCGGAGGCTAAACAGGAGCGCGATTTAAAGGATTTTAGACAGGAACGGTAGCCAGATC 916
Db 5434 GCGGAGGCTAAACAGGAGCGCGATTTAAAGGATTTTAGACAGGAACGGTAGCCAGATC 5375
QY 917 TTGAGAGTGTGTTTATTAATCAGTGAGCGCCACCGAGTAAAGAGTCTGTCATACGCAA 976
Db 5374 TTGAGAGTGTGTTTATTAATCAGTGAGCGCCACCGAGTAAAGAGTCTGTCATACGCAA 5315
QY 977 ATTAACCGTTGAGCAATACCTTCTTGTATTAGTAAATACATACATGCTGAGTGAAGA 1036
Db 5314 ATTAACCGTTGAGCAATACCTTCTTGTATTAGTAAATACATACATGCTGAGTGAAGA 5255
QY 1037 ACTAAACTATCGGCTTGTGGTAAATATCCAGAACATATATCCGCGCAGCATTTGCAAC 1096
Db 5254 ACTAAACTATCGGCTTGTGGTAAATATCCAGAACATATATCCGCGCAGCATTTGCAAC 5195
QY 1097 AGGAAAACGCTATGGAATACCTACATTTTGACGCTCAATCGCTGAAATGGATATT 1156
Db 5194 AGGAAAACGCTATGGAATACCTACATTTTGACGCTCAATCGCTGAAATGGATATT 5135
QY 1157 TACATTGSCAGATTACAGTACACAGCAGTAAATAAAGGGACATTTGCGCCCAACAGA 1216
Db 5134 TACATTGSCAGATTACAGTACACAGCAGTAAATAAAGGGACATTTGCGCCCAACAGA 5075
QY 1217 G 1217
Db 5074 G 5074

RESULT 14

US-08-349-131-2/c

; Sequence 2, Application US/08349131

; Patent No. 5871974

; GENERAL INFORMATION:

; APPLICANT: HUSE, WILLIAM D.

; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF

; TITLE OF INVENTION: HETEROMERIC RECEPTORS

; NUMBER OF SEQUENCES: 75

; CORRESPONDENCE ADDRESS:

; ADDRESS: PRETTY, SCHROEDER, BRUGGEMANN & CLARK

; STREET: 444 SO. FLOWER STREET, SUITE 200

; CITY: LOS ANGELES

; STATE: CALIFORNIA

; COUNTRY: UNITED STATES

; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/349,131
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/120,648
; FILING DATE:
; APPLICATION NUMBER: US/07/767,136
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8882
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001
; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-349-131-2

Query Match

93.0%; Score 1131.4; DB 2; Length 7317;

Best Local Similarity 99.5%; Pred. No. 2e-242;

Matches 1135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 77 CTGTTTCCTGTGTGAAATGTTATCGCTCACAAATCCACACACATACGAGCGGAGC 136
Db 6214 CTCTTTGGGCTGTGAAATGTTATCGCTCACAAATCCACACACATACGAGCGGAGC 6155
QY 137 ATAAAGTGTAAAGCCCTGGGTGCTTAATGAGTGAGCTAACTCACTTAATTTGCGTTGCGC 196
Db 6154 ATAAAGTGTAAAGCCCTGGGTGCTTAATGAGTGAGCTAACTCACTTAATTTGCGTTGCGC 6095
QY 197 TCACCTCCGCTTTCCAGTCGGGAAACCTCTGTCGCGAGCTGCAATTAATGAATCGGCAA 256
Db 6094 TCACCTCCGCTTTCCAGTCGGGAAACCTCTGTCGCGAGCTGCAATTAATGAATCGGCAA 6035
QY 257 CGCGCGGGGAGAGCGGCTTTGCGCTATTTGGCGCCAGGCTGTTTCTTTTCCACAGTGA 316
Db 6034 CGCGCGGGGAGAGCGGCTTTGCGCTATTTGGCGCCAGGCTGTTTCTTTTCCACAGTGA 5975
QY 317 GACGGGCAACAGCTGATTGCGCTTTACCGCTTGCCCTGAGAGAGTTGCAGCAAGCGGTC 376
Db 5974 GACGGGCAACAGCTGATTGCGCTTTACCGCTTGCCCTGAGAGAGTTGCAGCAAGCGGTC 5915
QY 377 CAGCTGGTTTGGCCAGCAGGCGAAATCCTGTTTGTATGGTGTTCGGAATCGGAAA 436
Db 5914 CAGCTGGTTTGGCCAGCAGGCGAAATCCTGTTTGTATGGTGTTCGGAATCGGAAA 5855
QY 437 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTTCAGTTTGAAC 496
Db 5854 ATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGTTGAGTGTTCAGTTTGAAC 5795
QY 497 AAGAGTCCACTATTAAAGAACGTGGACTCCAACGCTAAAGGGCGGAAACCGCTATCAG 556
Db 5794 AAGAGTCCACTATTAAAGAACGTGGACTCCAACGCTAAAGGGCGGAAACCGCTATCAG 5735
QY 557 GCGGATGGCCCTACTAGCTGAACCATCACCAATCAAGTTTGTGGGTTCAGGTTGCGCT 616
Db 5734 GCGGATGGCCCTACTAGCTGAACCATCACCAATCAAGTTTGTGGGTTCAGGTTGCGCT 5675
QY 617 AAAGCACTAAATCGGAACCCCTAAAGGAGCGCCCGATTTAGAGCTTGACGGGAAAGCGG 676
Db 5674 AAAGCACTAAATCGGAACCCCTAAAGGAGCGCCCGATTTAGAGCTTGACGGGAAAGCGG 5615

QY 677 GCGAAGCTGGCGAGAAAGGAAGGAAGAAAGCGAAGAGAGCGGGCGCTAGGCGCTGGCA 736
|||||
Db 5614 GCGAAGCTGGCGAGAAAGGAAGGAAGAAAGCGAAGAGAGCGGGCGCTAGGCGCTGGCA 5555
QY 737 AGTGTAGCGGTCACGCTGCGGTACACACACACCGCGCGCTTAATCGCGCTACAG 796
|||||
Db 5554 AGTGTAGCGGTCACGCTGCGGTACACACACACCGCGCGCTTAATCGCGCTACAG 5495
QY 797 GCGCGTACTATGTTGCTTTGAGCAGCAGCTATTAACGTGCTTCTCGTTGGAATCAGA 856
|||||
Db 5494 GCGCGTACTATGTTGCTTTGAGCAGCAGCTATTAACGTGCTTCTCGTTGGAATCAGA 5435
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QY 917 TTGAGAAGTGTGTTTATTAATCAGTGAGCGCCAGGTAAGAGAGTCTGCTCATCAGCAA 976
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QY 977 ATTAACCGTTGTAGCAATCTCTTTGATTAGTAATAACATCACCTTGCCTGAGTAGAAGA 1036
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Db 5314 ATTAACCGTTGTAGCAATCTCTTTGATTAGTAATAACATCACCTTGCCTGAGTAGAAGA 5255
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QY 1097 AGGAAAACGCTCATGGAATACCTACATTTTGAGCTCAATCTGCTGAAATGGATTAT 1156
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QY 1157 TACATTGGCAGATTCACAGTCAACAGCACAGTAAATAAGAGGACATCTGGCCCAACAGA 1216
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Db 5134 TACATTGGCAGATTCACAGTCAACAGCACAGTAAATAAGAGGACATCTGGCCCAACAGA 5075
QY 1217 G 1217
Db 5074 G 5074

RESULT 15

US-08-470-297A-2/C
; Sequence 2, Application US/08470297A
; Patent No. 6027933
; GENERAL INFORMATION:
; APPLICANT: HUSE, WILLIAM D.
; TITLE OF INVENTION: SURFACE EXPRESSION LIBRARIES OF
; HETEROMERIC RECEPTORS
; NUMBER OF SEQUENCES: 76
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES LLP
; STREET: 4370 LA JOLLA VILLAGE DRIVE, SUITE 700
; CITY: SAN DIEGO
; STATE: CALIFORNIA
; COUNTRY: UNITED STATES
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,297A
; FILING DATE: June 5, 1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: CAMPBELL, CATHRYN A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-IX 1611
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-535-9001

; TELEFAX: 619-535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7317 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: circular
; US-08-470-297A-2

Query Match 93.0%; Score 1131.4; DB 3; Length 7317;
Best Local Similarity 99.5%; Pred. No. 28-242;
Matches 1135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 77 CTGTTTCTGTTGTAATTTGTTATCCGCTCACAATTTCCACACAATACACGCGGAAGC 136
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Db 6214 CTCCTTGGCGTGTGAATTTGTTATCCGCTCACAATTTCCACACAATACACGCGGAAGC 6155
QY 137 ATAAAGTGAAGGCTTGGGTGCTTAATGAGTGAGCTAACTCACAATTAATTTGGTTTCGC 196
|||||
Db 6154 ATAAAGTGAAGGCTTGGGTGCTTAATGAGTGAGCTAACTCACAATTAATTTGGTTTCGC 6095
QY 197 TCACCTGCGGCTTTCCAGTCGCGGAACCTGTCGTCGCACTGCATTAATGAATCGGCCAA 256
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Db 5494 GCGCGCTACTATGTTGCTTTGAGCAGCAGCTATTAACGTGCTTCTCGTTGGAATCAGA 5435
QY 857 GCGGAGCTAAACAGGAGCGGATTAAGGGATTTAGACAGGAACGGTACGCCAGAATC 916
|||||
Db 5434 GCGGAGCTAAACAGGAGCGGATTAAGGGATTTAGACAGGAACGGTACGCCAGAATC 5375
QY 917 TTGAGAAGTGTGTTTATTAATCAGTGAGCGCCAGGTAAGAGAGTCTGCTCATCAGCAA 976
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Db 5374 TTGAGAAGTGTGTTTATTAATCAGTGAGCGCCAGGTAAGAGAGTCTGCTCATCAGCAA 5315

us-10-014-743-1.rni

Thu Aug 1 12:08:39 2002

QY 977 ATTAACCGTTGTAGCAATACTTCTTTGATTAGTAATACATCAGCTTGCTGAGTAGAGA 1036
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 Db 5194 AGCAAAACGCTCATGGAATACCTACATTTTGACGCTCAATCGTCTGAAATGGATTATT 5135
 QY 1157 TACATTGGCAGATTACCCAGTACAGCAGTAAATAAGGAGACATTCTGGCCCAACAGA 1216
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 QY 1217 G 1217
 Db 5074 G 5074

Search completed: August 1, 2002, 09:30:47
 Job time: 6608 sec

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 1, 2002, 06:51:49 ; Search time 2971.21 Seconds
(without alignments)
5528.318 Million cell updates/sec

Title: US-10-014-743-1
Perfect score: 1217
Sequence: 1 GCCAGCTTGATGCTGCA.....GGACATTCGTGGCCACAGAG 1217

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*
1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmd.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_estl.*
10: gb_est2.*
11: gb_hic.*
12: gb_gss.*
13: em_gss_hum.*
14: em_gss_inv.*
15: em_gss_pln.*
16: em_gss_vrt.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	555.4	45.6	687	12	AQ937512 NB6-1069C
2	497.4	40.9	632	10	BI795424 H021C07 E
3	452.4	37.2	478	9	AU014102 AU014102
4	450.2	37.0	571	12	FR0010806
5	433.6	35.6	564	12	AL002058 F.rubripe
6	394.6	32.4	770	12	AQ991774 Rfc02039F
7	387.2	31.8	588	12	FR0010785
8	383.4	31.5	677	12	TA2308P
9	379.6	31.2	611	9	AJ273684
10	379	31.1	554	12	BH216739
11	379	31.1	556	12	BH231528
12	379	31.1	581	9	AV403804
13	379	31.1	584	9	AV404063
14	379	31.1	627	9	AV403998
15	379	31.1	627	9	AV404060
16	379	31.1	627	9	AV404091
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20	379	31.1	628	9	AV403918
21	379	31.1	628	9	AV403919
22	379	31.1	628	9	AV403945
23	379	31.1	628	9	AV403970
24	379	31.1	628	9	AV403997
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29	379	31.1	684	9	AV404405
30	379	31.1	690	9	AV405131
31	379	31.1	713	9	AV403818
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34	379	31.1	756	9	AV404290
35	379	31.1	783	9	AV402901
36	379	31.1	786	9	AV404165
37	379	31.1	799	9	AV405326
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39	378.4	31.1	844	12	AQ115013
40	378.4	31.1	654	12	B78704
41	378.4	31.1	659	12	BH244704
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43	378.4	31.1	838	12	AZ687181
44	378.4	31.1	841	12	A2541344
45	378.4	31.1	865	12	AZ670321

ALIGNMENTS

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DEFINITION AQ937512
ACCESSION AQ937512
VERSION AQ937512.1 GI:7213890
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 687)
AUTHORS Zabarovsky,E.R., Gizatullin,R., Podowski,R.M., Zabarovska,V.V., Xie L., Muravenko,O.V., Kozirev,S., Petrenko,L., Skobeleva,N., Li,J., Protopopov,A., Kashuba,V., Ernberg,I., Winberg,G. and Wahlestedt,C.
TITLE NotI clones in the analysis of the human genome
JOURNAL Nucleic Acids Res. 28 (7), 1635-1639 (2000)
MEDLINE 20175728
COMMENT Contact: Podowski RM
Center for Genomics Research
Karolinska Institute
17177 Stockholm, Sweden
Tel: +46-8-728-6372
Fax: +46-8-337983
Email: Raf.Podowski@cgr.ki.se
Class: NotI site.
location/Qualifiers
source
1. .687
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="Human NotI clones"
BASE COUNT 168 a 170 c 187 g 162 t
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Query Match 45.6%; Score 555.4; DB 12; Length 687;
Best Local Similarity 99.1%; Pred. No. 2.2e-148;
Matches 570; Conservative 0; Mismatches 1; Indels 4; Gaps 1;
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Db 113 ATGATCCCGGGTACCGAGCTCGAATTAATCGTAAATCATGTGTCATAGCTGTTCTCTGTG 172
QY 89 TGAATTTGTTATCGCTCACAAATTCACACACATACAGCGCGGAAGCATAAAGTGTAA 148
Db 173 TGAATTTGTTATCGCTCACAAATTCACACACATACAGCGCGGAAGCATAAAGTGTAA 232
QY 149 GCCTGGGGTGCTTAATGAGTGAAGTCAATTAATGCGTTGCGGTCACTGCCCGCT 208
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QY 329 CTGATTCGCCCTTACCGGCTGGCCCTGAGAGAGTTGTCAGAGCGGTCCACGCTGGTTTG 388
Db 413 CTGATTCGCCCTTACCGGCTGGCCCTGAGAGAGTTGTCAGAGCGGTCCACGCTGGTTTG 472
QY 389 CCCAGCAGCGGAATCCTGTTTCATGCTGTTTCGTTCCGAAATCGGCAAAATCCCTTATAA 448
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QY 569 CTAGCTGAACCATCACCAATCAAGTTTGTGG 603
Db 653 CTAGCTGAACCATCACCAATCAAGTTTGTGG 687

RESULT 2
BI795424/c
LOCUS
DEFINITION
H021C07 Endosperm library from Oryza sativa (10 days after anthesis
) Oryza sativa cDNA clone H021C07, mRNA sequence.
ACCESSION
BI795424
VERSION
BI795424.1 GI:15847148
KEYWORDS
EST.
SOURCE
Oryza sativa.
ORGANISM
Oryza sativa.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 632)
AUTHORS
Dong, H.T., Li, D.B., Zhuang, X.F., Dai, C.G., Sun, L.X., Pei, Y.X., Wu
H.F., Jiang, Y.X., Yu, F.C., Gao, Q.K. and Lou, Y.C.
TITLE
A Gene Expression Screen in Oryza sativa
JOURNAL
Unpublished (2001)
COMMENT
Contact: Dong HT
Laboratory of Functional Genetics
Bio-technology Institute of Zhejiang University
Kaixuan Road 268# Hangzhou, Zhejiang, P.R.China
Tel: 0086-571-86892051
Fax: 0086-571-86961525
Email: htdong@zjuem.zju.edu.cn
Seq primer: M13 forward primer.
FEATURES
Location/Qualifiers
1..632
/organism="Oryza sativa"
/db_xref="taxon:4530"
/clone="H021C07"
/gene="H021C07"
after anthesis")
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/dev_stage="10 days after anthesis"
/note="Vector: pSport2"
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Best Local Similarity 93.7%; Pred. No. 9.9e-132;
Matches 595; Conservative 0; Mismatches 31; Indels 9; Gaps 7;

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Db 571 GCTGTTTCTCTGTCGCAAAATGTTATCCCGCTCAAAATTCACACACATACGAGCGCGAAG 512
QY 136 CATAAAGTGTAAAGCTGGGTGCTTAATGAGTGAAGTCAACTCACATTAATTCGTTGCG 195
Db 511 CATAAAGTGTAAAGCTGGGTGCTTAATGAGTGAAGTCAACTCACATTAATTCGTTGCG 452
QY 196 CTCAGTCCCGCTTTCCAGTCCGGGAACCTGTCGTGCCAGCTGCATTAATGAATTCGCCA 255
Db 451 CTCAGTCCCGCTTTCCAGTCCGGGAACCTGTCGTGCCAGCTGCATTAATGAATTCGCCA 392
QY 256 ACAGCGGGGAGAGCGGTGTCGTTATTCGGCGCCAGGCTGTTTCTTTTCCACCACTG 315
Db 391 ACAGCGGGGAGAGCGGTGTCGTTATTCGGCGCCAGGCTGTTTCTTTTCCACCACTG 332
QY 316 AGACGGGCAACAGCTGATTGCTTACCGCTTCAGAGAGTTCGAGAGTTCGAGCAAGCGGT 375
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QY 376 CCAGCTGCTTTGCCCGAGCGGCAAAATCTCTGTTGATGTTGTTTCCGAAATTCGCCAA 435
Db 274 CCAGCTGCTTTGCCCGAGCGGCAAAATCTCTGTTGATGTTTCCGAAATTCGCCAA 216
QY 436 AATCCCTTATAAATCAAAAGATAGCGGATAGGTTGAGTGTGTTGTTCCAGTTTGGAA 495
Db 215 AATCCCTTATAAATCAAAAGATAGCGGATAGGTTGAGTGTGTTTCCAGTTTGGAA 156
QY 496 CAAGAGTCCACTATTAAAGAGAGTGGACTTCCAAAGTCAAAAGGCGGAAACCGCTCTATCA 555
Db 155 CAAGAGTCCACTATTAAAGAGAGTGGACTTCCAAAGTCAAAAGGCGGAAACCGCTCTATCA 98
QY 556 GGGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTCGGGGTCGAGGTGCGG 615
Db 97 GG--CGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTCGGGGTCGAGGTGCGG 40
QY 616 TAAAGCACTAAATCGGAACCCCTAAAGGGAGGAGCCCC 650
Db 39 GTAGCACTAAATCGGAACCCCTTAAGGGAGGAGCCCC 5

RESULT 3
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LOCUS
DEFINITION
AU014102 Schizosaccharomyces pombe late log phase cDNA
Schizosaccharomyces pombe cDNA clone spc09168, mRNA sequence.
ACCESSION
AU014102
VERSION
AU014102.1 GI:3368893
KEYWORDS
EST.
SOURCE
fission yeast.
ORGANISM
Schizosaccharomyces pombe
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
Schizosaccharomyces.
REFERENCE
1 (bases 1 to 478)
AUTHORS
Morimyo, M. and Mita, K.
TITLE
Identification of expressed sequence tags of Schizosaccharomyces
pombe
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VERSION      AL002058.1  GI:2447628
KEYWORDS     GSS; genome survey sequence.
SOURCE       Takifugu rubripes.
ORGANISM     Takifugu rubripes
              Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
              Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
              Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
              Tetraodontidae; Takifugu.
REFERENCE    1 (bases 1 to 564)
AUTHORS      Elgar, G., Clark, M., Smith, S., Meek, S., Warner, S., Umrana, Y.,
              Williams, G. and Brenner, S.
TITLE        Direct Submission
JOURNAL      Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
              Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hgm.mrc.ac.uk
COMMENT      Vector: m3mpl18
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417 TAAACCAACACACCCCGCGCTTAATGCGCGCTACAGGCGCGGTACTATGTTGC-TT 475
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817 TGACGAGCAGTATAAGCTGCTTTCCTCGTTGGAAT--CAGAGCGGAGGTAACAGGAG 874
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476 TGACGAGCAGTATAAGCTGCTTTCCTCGTTGGAAT--CAGAGCGGAGGTAACAGGAG 901
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875 G--CCGATTAAAGGGATTTAGACAGGAA 901
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536 GGCCCGGATTAAAGGGATTTAGACAGGAA 564
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RESULT 6

AQ991774

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

COMMENT

770 bp DNA linear GSS 14-AUG-2000
 Rf02039F Photorhabdus luminescens strain W14 M13 library
 Photorhabdus luminescens genomic clone PLG02039F, DNA sequence.
 AQ991774
 AQ991774
 AQ991774.1 GI:9650368
 GSS.
 Photorhabdus luminescens.
 Photorhabdus luminescens.
 Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 Photorhabdus.
 1 (bases 1 to 770)
 fFrench-Constant, R.H., Waterfield, N., Burland, V., Perna, N.T.,
 Daborn, P.J., Bowen, D. and Blattner, F.R.
 A genomic sample sequence of the entomopathogenic bacterium
 Photorhabdus luminescens W14; potential implications for virulence
 Appl. Environ. Microbiol. 66 (8), 3310-3329 (2000)
 20378633
 Contact: fFrench-Constant RH
 Department of Biology and Biochemistry
 University of Bath
 South Building, Bath BA2 7AY, UK
 Tel: (44) 1225 826621
 Fax: (44) 1225 826779
 Email: bssrfc@bath.ac.uk
 This is one of a selected subset of flipped clones from the M13
 library. For annotation of identified clones (BLASTX, BLASTN and
 mapping to E. coli K12 genome) please see fFrench-Constant et al.
 2000, Nucleic Acids Res.
 Seq primer: M13 Reverse
 Class: shotgun.

FEATURES

source

Location/Qualifiers

1..770

/organism="Photorhabdus luminescens"

/strain="W14"

/db_xref="taxon:29488"

/clone="PLG02039F"

/clone_lib="Photorhabdus luminescens strain W14 M13 library"

/dev_stage="primary phase variant"

/note="Genomic DNA from strain W14 was size selected (1-2 kb) and then cloned into M13 Janus."

BASE COUNT

238 a 166 c 178 g 165 t 23 others

ORIGIN

Query Match

Best Local Similarity

Matches 478; Conservative

0; Mismatches 74; Indels 11; Gaps 4;

Qy 368 CAAGCGTCCAGCGTGGTTGCCCCAGCAGCGGAAATCCTGTTGATCGTGGTCCGAA 427

Db 209 CAAGCTGTCCAGCTGGTTGCCCCAGCAGCGGAAATCCTGTTGATCGTGGTCCGAA 268

Qy 428 ATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGTTGAGTGTGTTCCA 487

Db 269 ATCGCAAAATCCCTTATAAATCAAAAGAAATAGCCCGAGATAGGTTGAGTGTGTTCCA 328

Qy 488 GTTTGGACAAAGTCCACTATTAAAGAACGTGGGACTCCAAGCTCAAGGGCGGAAACCC 547

Db 329 GTTTGGACAAAGTCCACTATTAAAGAACGTGGGACTCCAAGCTCAAGGGCGGAAACCC 388

Qy 548 GTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCAATCAAGTTTGTGGGTGCG 607

Db 389 GTCTATCAGGGCGATGGCCCACTACGTGAACCATCACCAATCAAGTTTGTGGGTGCG 448

Qy 608 AGGTGCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCCGGATTTAGAGCTTTGACGG 667

Db 449 AGGNGCCGTAAAGCACTAAATCGGAACCCCTAAAGGGAGCCCCCGGATTTAAAGCTTTGACGG 508


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QY 668 GGAAGCCGCGCAACGTCGGCAGAAAGGAGGAAAGCAAGAGGAGCGGCGCTAGG 727
DB 509 GGAAGCCGCGCAACGTCGGCAGAAAGGAGGAAAGCAAGAGGAGCGGCGCTAGG 568
QY 728 GCGCTGCGCAAGTGTAGCGGTACGCTGCGCTAACCACACCGCGCGCTTAATGCG 787
DB 569 GC-----CTGCAAGTGTANCGGACCCCTGGCTAACCACCGCGCTTAATGCG 620
QY 788 CCGCTACAGGCGCGCTACTATGTTGCTTTGACGAGCAGCTATACGTCCTTCCTGCTT 847
DB 621 CCCCTTCANGGCGGT-CTATGTTGTTT-ACNAGCACCTATAACGTCCTTTCTTTT 678
QY 848 GGAATCAGAGCGGCGAGCTTAACAGCAGGCGGCTTTAAAGGATTTTAGACAGCAACGATC 907
DB 679 AGAATNAAGCGGCGCTTTAAANAGGCGCCNTTTAAAGGCGTTT-NACAGACCGGNC 737
QY 908 GCCAGAATCTTGAGAAGTGT 930
DB 738 CCCAATCTGNAAGGTTT 760

RESULT 7
FR0010785 588 bp DNA linear GSS 18-SEP-1997
LOCUS F.rubripes GSS sequence, clone 045G19a7, genomic survey sequence.
ACCESSION AL002056
VERSION AL002056.1 GI:2447626
KEYWORDS GSS; genome survey sequence.
SOURCE Takifugu rubripes
ORGANISM Takifugu rubripes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
REFERENCE 1 (bases 1 to 588)
AUTHORS Elgar,G., Clark,M., Smith,S., Meek,S., Warner,S., Umrana,Y.,
Williams,G. and Brenner,S.
TITLE Direct Submission
JOURNAL Submitted (09-SEP-1997) MRC Human Genome Mapping Project Resource
Centre Hinxton, Cambridge, CB10 1SB. Email: biohelp@hmp.mrc.ac.uk
COMMENT Vector: m13mp18
V_type: phage
PRIMER: M13
DESCR: One pass dye-terminator sequencing of cosmid cloned genomic
sequence.
FEATURES             Location/Qualifiers
     source            1..588
     /organism="Takifugu rubripes"
     /db_xref="taxon:31033"
     /clone_lib="cosmid 045G19"
     /clone_1="045G19a7"
BASE COUNT 168 a 127 c 159 g 123 t 11 others
ORIGIN
Query Match 31.8%; Score 387.2; DB 12; Length 588;
Best Local Similarity 87.5%; Pred. No. 4.3e-100;
Matches 498; Conservative 0; Mismatches 52; Indels 9; Gaps 7;

QY 463 CGAGATAGGGTTGAGTGTGTCAGTTTGGACAAGAGTCCACTATTAAAGACGTGGA 522
DB 1 CGAGATAGGGTTGAGTGTGTCAGTTTGGACAAGAGTCCACTATTAAAGACGTGGA 60
QY 523 CTCACAGTCAAGGGCGAAGAAACCGTCTATCAGGCGGATGCCACCTACGTGAACCATC 582
DB 61 CTCACAGTCAAGGGCGAAGAAACCGTCTATCAGGCGGATGCCACCTACGTGAACCATC 118
QY 583 ACCCAATCAAGTGTGTTGGGCGTCGAGTGCCTGCGGTAAGCACTAAATCGGAACCCCTAAAGG 642
DB 119 ACCCAATCAAGTGTGTTGGGCGTCGAGTGCCTGCGGTAAGCACTAAATCGGAACCCCTAAAGG 178
QY 643 GAGCCCCCGATTTAGAGCTTGACGGGGAAGCGCGCG-ACGTCGGCAGAAAGGAGGGA 701

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DB 179 GAGCCCCCGATTTAGAGCTTGACGGGAAAGCCGCGAAACGTCGGCAGAAAGGGA 238
QY 702 AGAAGCGAAAGAGCGGCGCTAGGCGCTGCAAGTGTAGCGGTACACCTCGCGCTAA 761
DB 239 AGAAGCGAAAGAGCGGCGC-CTAGGGCTGTGCAAGTGTAGCGGTTCACCTGCGGNTAA 297
QY 762 CCACCACACCGCGCGCTTAATGCGCGCTACAGGCGCGCTACTATGTTGCTTTGACG 821
DB 298 ACCACACACCGCGCGCTTAATGCGCGCTACAGCGCTAACTATGTTGCTTTGACG 357
QY 822 AGCAGCTATAACGTCGTTCTCGTTGGAATCAGAGCGGAGCTAAACAGAGGCCGAT 881
DB 358 AGCAGCTATAACGTTTCTCTCGTAG--ATCAGAGCGGAGTAAACAGAGGCCGAT 415
QY 882 AAAGGATTTTACACAGGAACGCTACCCAGAACTCTTGAGAAGTGTGTTTATAATCACTG 941
DB 416 AAAGGATTTTACACAGGAACGCTACCCAGAACTCTTGAGAAGTGTGTTTATAATCACTG 474
QY 942 AGCCACCGAGTAAAGAGTCTGTCCATCAGC-CAAAATTAACCGTTGTAGCAACTTCT 1000
DB 475 AGCCACCGAGTAAAGAGTCTGTCCATCAGC-CAAAATTAACCGTTGTAGCAACTTCT 534
QY 1001 TTGATTAGTAAATACATCACTTGCTGAG 1029
DB 535 TTGATTAG-NATAACANCACTTGCCCTGAG 562

RESULT 8
TA2G08P 677 bp DNA linear GSS 16-SEP-2000
LOCUS T. brucei sheared genomic DNA clone 2908, forward sequence, similar
DEFINITION to AR036903 AR036903 Sequence 1 from patent US 5800996. . . ., N-1907,
Prob=5.1e-151, genomic survey sequence.
ACCESSION AL441673
VERSION AL441673.1 GI:10185362
KEYWORDS GSS.
SOURCE Trypanosoma brucei.
ORGANISM Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma.
REFERENCE 1 (bases 1 to 677)
AUTHORS Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R.,
Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L.,
Melville,S.E., Rajandream,M.A. and Barrell,B.G.
TITLE Direct Submission
JOURNAL Submitted (15-SEP-2000) Trypanosoma brucei genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrellesanger.ac.uk and
nhl@sanger.ac.uk
COMMENT Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
to give a tight size distribution (
4 kb). The v-i method used for the library construction is
described in detail in Smith, H. and Venter, J.C. (Making small
insert libraries for whole genome shotgun sequencing projects. In
Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barrell, Oxford University Press, 1999).
Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available
at http://www.sanger.ac.uk/projects/T_brucei/.
FEATURES             Location/Qualifiers
     source            1..677
     /organism="Trypanosoma brucei"
     /strain="TREU927"
     /db_xref="taxon:5691"
     /clone="2908"
BASE COUNT 175 a 162 c 187 g 148 t 5 others
ORIGIN
Query Match 31.5%; Score 383.4; DB 12; Length 677;

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Db	193	CGAAATCGGCAAAATCCCTTATTAATCAAAGAATAGACCGGATAGGGTTGAGTGTG	252
Qy	483	TTCCAGTTTGGAAACAAGATCCACTATTAAAGAACGTGGACTCCAAGCTCAAGAGCGGAA	542
Db	253	TTCCAGTTTGGAAACAAGATCCACTATTAAAGAACGTGGACTCCAAGCTCAAGAGCGGAA	312
Qy	543	AAACCGTCTATCAGGGCGGATGGCCCACTAGTGAAACCATCACCCAAATCAAGTTTTTGG	602
Db	313	AAACCGTCTATCAGGGCGGATGGCCCACTAGTGAAACCATCACCCATCAAGTTTTTGG	372
Qy	603	GGTCAGGTCCGTAAAGCACTAAATCGGAACCTTAAGAGGACCCCGATTTAGAGCTT	662
Db	373	GGTCAGGTCCGTAAAGCACTAAATCGGAACCTTAAGAGGACCCCGATTTAGAGCTT	432
Qy	663	GACGGGAAGCCGGCGAAGCTGGCGAGAAAGGAAGGAAAGGACGCGGGG	722
Db	433	GACGGGAAGCCGGCGAAGCTGGCGAGAAAGGAAGGAAAGGACGCGGGG	492
Qy	723	CTAGGGCGCTGGCAAGTGTAGCGGTACGCTGGCGGTAAACCACACCCGCCCTTA	782
Db	493	CTAGGGCGCTGGCAAGTGTAGCGGTACGCTGGCGGTAAACCACACCCGCCCTTA	552
Qy	783	ATGCGGGCTACAGGGCGGCTACTATGGTTGCTTT	817
Db	553	ATGCGGGCTACAGGGCGGCTCANGTGGCACTTT	587

1000040411.X1.1006	RescueMu Grid G Zea mays genomic, DNA sequence.
BH216739	
BH216739.1	GI:16807535
GSS.	
SOURCE	zea mays.
ORGANISM	zea mays.
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
AUTHORS	1 (bases 1 to 554)
TITLE	Walbot,V.
JOURNAL	Maize genomic sequences found using engineered RescueMu transposon
COMMENT	Unpublished (2001) Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221

Possible ligation site of ends cut by 2 different endonucleases.
 Reverse complemented post-ligation sequence from source sequence.
 Plate: 1006046 row: 3
 Class: transposon-tagged.
 Location/Qualifiers
 source 1..554

RescueMu (puc19 backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmndb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI

and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin." 163 a 123 c 146 g 122 t

BASE COUNT
ORIGIN

Query Match 31.1%; Score 379; DB 12; Length 554;
Best Local Similarity 97.5%; Pred. No. 9.6e-98;
Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 423 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 482
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Db 75 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 134
QY 483 TTCCAGTTTGGAAACAGAGTCCATTAATTAAGACGTGGACTCCCAACGTCAAGGGCGAA 542
|||||
Db 135 TTCCAGTTTGGAAACAGAGTCCATTAATTAAGACGTGGACTCCCAACGTCAAGGGCGAA 194
QY 543 AAACCGTCTATCAGGGGATGGCCCACTACCTGAACCATCAACCAAAATCAAGTTTGTG 602
|||||
Db 195 AAACCGTCTATCAGGGGATGGCCCACTACCTGAACCATCAACCAAAATCAAGTTTGTG 254
QY 603 GGTGAGGTGCGGTAAGACACTAATCGGAACCTTAAGAGGAGCGCCCGATTTAGAGCTT 662
|||||
Db 255 GGTGAGGTGCGGTAAGACACTAATCGGAACCTTAAGAGGAGCGCCCGATTTAGAGCTT 314
QY 663 GACGGGAAACCGCGGACGTGGCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
|||||
Db 315 GACGGGAAACCGCGGACGTGGCGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGG 374
QY 723 CTAGGGCGCTGCGAAGTGTACGGTTCAGCTGCGGTAAACACACACACCGCGGCTTA 782
|||||
Db 375 CTAGGGCGCTGCGAAGTGTACGGTTCAGCTGCGGTAAACACACACACCGCGGCTTA 434
QY 783 ATGCGCGCTACAGGGCGGCTACTGTTGCTTT 817
|||||
Db 435 ATGCGCGCTACAGGGCGGCTACTGTTGCTTT 469

RESULT 11
BH231528 556 bp DNA linear GSS 08-NOV-2001
LOCUS 1006162F02.x1 1006 - RescueMu Grid G Zea mays genomic, DNA
DEFINITION
sequence.
ACCESSION BH231528
VERSION BH231528.1 GI:16835766
KEYWORDS GSS.
SOURCE Zea mays.
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoidae; Andropogoneae; Zea.
1 (bases 1 to 556)
Walbot, V.
Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.
Plate: 1006162 row: 19
Class: transposon-tagged.
Location/Qualifiers
1. .556
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Maize genomic sequences found using engineered RescueMu transposon Unpublished (2001)
Contact: Walbot V
Department of Biological Sciences
Stanford University
855 California Ave, Palo Alto, CA 94304, USA
Tel: 650 723 2227
Fax: 650 725 8221
Email: walbot@stanford.edu
possible ligation site so sequence was trimmed. Post-ligation sequence submitted separately.
Plate: 1006162 row: 19
Class: transposon-tagged.
Location/Qualifiers
1. .556
/organism="Zea mays"
/cultivar="mixed background W23/A188/B73"
/db_xref="taxon:4577"

/clone_lib="1006 - RescueMu Grid G"
/tissue_type="leaf"
/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: Leaf; Vector: RescueMu (engineered from pBlueScript backbone); Site_1: BamHI; Site_2: BglII; RescueMu is a 4.9 kb, modified maize Mu transposon designed to allow plasmid rescue from total genomic DNA. Mu elements insert preferentially into transcription units. For more information on RescueMu, go to the web site 'www.zmndb.iastate.edu' and follow the links for 'RescueMu.' Grid G was grown at Stanford in 2000. DNA was extracted from leaf punches, double digested using BamHI and BglII, and ligated to form circular plasmids. DH10B cells were transformed and then screened on LB plates with ampicillin." 160 a 121 c 145 g 128 t 2 others

BASE COUNT 160 a 121 c 145 g 128 t 2 others
ORIGIN
Query Match 31.1%; Score 379; DB 12; Length 556;
Best Local Similarity 97.5%; Pred. No. 9.6e-98;
Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
QY 423 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 482
|||||
Db 96 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 155
QY 483 TTCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGGACTCCCAACGTCAAGGGCGAA 542
|||||
Db 156 TTCCAGTTTGGAAACAGAGTCCACTATTAAAGAACGTGGACTCCCAACGTCAAGGGCGAA 215
QY 543 AAACCGTCTATCAGGGGATGGCCCACTACCTGAACCATCAACCAAAATCAAGTTTGTG 602
|||||
Db 216 AAACCGTCTATCAGGGGATGGCCCACTACCTGAACCATCAACCAAAATCAAGTTTGTG 275
QY 603 GGTGAGGTGCGGTAAGACACTAAATCGGAACCTTAAGGGAGGCGCCGCTTTAGAGCTT 662
|||||
Db 276 GGTGAGGTGCGGTAAGACACTAAATCGGAACCTTAAGGGAGGCGCCGCTTTAGAGCTT 335
QY 663 GACGGGAAACCGCGGACGTGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
|||||
Db 336 GACGGGAAACCGCGGACGTGGCGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 395
QY 723 CTAGGGCGCTGCGAAGTGTACGGTTCAGCTGCGGTAAACACACACACCGCGGCTTA 782
|||||
Db 396 CTAGGGCGCTGCGAAGTGTACGGTTCAGCTGCGGTAAACACACACACCGCGGCTTA 455
QY 783 ATGCGCGCTACAGGGCGGCTACTGTTGCTTT 817
|||||
Db 456 ATGCGCGCTACAGGGCGGCTACTGTTGCTTT 490

RESULT 12
AV403804 581 bp mRNA linear EST 06-FEB-2000
LOCUS AV403804 Bombyx mori pheromone gland Shuko x Ryuhaku newly-closed
DEFINITION adult Bombyx mori cDNA clone pg--0075 T3, mRNA sequence.
ACCESSION AV403804
VERSION AV403804.1 GI:6907892
KEYWORDS EST.
SOURCE domestic silkworm.
ORGANISM Bombyx mori
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.
1 (bases 1 to 581)
Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences

Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
 Email: knita@nirs.go.jp
 Method: uni-directional, sequence direction: sequenced from T3 primer
 (5' -> 3')
 Project: 'Silkworm Genome Program in MAFF, and Research for the
 Future Program in JSPS'. see 'SilkBase',
 <http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.
 Location/Qualifiers

FEATURES

source

1. 581
 /organism="Bombyx mori"
 /strain="Shuko x Ryuhaku"
 /db_xref="taxon:7091"
 /clone="pg-0075"
 /clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku
 newly-enclosed adult"
 /sex="female"
 /tissue_type="pheromone gland"
 /dev_stage="newly-enclosed adult"
 166 a 131 c 151 g 133 t

BASE COUNT

ORIGIN

Query Match 31.1%; Score 379; DB 9; Length 581;
 Best Local Similarity 97.5%; Pred. No. 9.8e-98;
 Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 423 CCGAAATCGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 482
 Db 116 CCGAAATCGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 175
 QY 483 TTCCAGTTTGAACAGAGTCCACTATTAAAGAGCTGGACTCCCAAGTCAAGGCGAA 542
 Db 176 TTCCAGTTTGAACAGAGTCCACTATTAAAGAGCTGGACTCCCAAGTCAAGGCGAA 235
 QY 543 AAACCGTCTATCAGGGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTGG 602
 Db 236 AAACCGTCTATCAGGGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTGG 295
 QY 603 GGTGAGGTGCGGTAAGAGCTAAATCGAACCCCTAAAGGAGAGCCCGGATTTAGAGCTT 662
 Db 296 GGTGAGGTGCGGTAAGAGCTAAATCGAACCCCTAAAGGAGAGCCCGGATTTAGAGCTT 355
 QY 663 GACGGGAAAGCGCGCAAGTGTAGCGGTACGCTGCGCGTAAACCAACACCCGCGCGCTTA 722
 Db 356 GACGGGAAAGCGCGCAAGTGTAGCGGTACGCTGCGCGTAAACCAACACCCGCGCGCTTA 415
 QY 723 CTAGGCGCTGCGCAAGTGTAGCGGTACGCTGCGCGTAAACCAACACCCGCGCGCTTA 782
 Db 416 CTAGGCGCTGCGCAAGTGTAGCGGTACGCTGCGCGTAAACCAACACCCGCGCGCTTA 475
 QY 783 ATGCGCGCTACAGGGCGCGTACTATGTTGCTTT 817
 Db 476 ATGCGCGCTACAGGGCGCGTACTATGTTGCTTT 510

RESULT 13

AV404063

LOCUS

AV404063 Bombyx mori pheromone gland Shuko x Ryuhaku linear EST 06-FEB-2000
 adult Bombyx mori cDNA clone pg-0399 T3, mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Contact: Mita K

Genome Research Group

National Institute of Radiological Sciences

Anagawa 4-9-1, Inage, Chiba 263-8555, Japan

Email: knita@nirs.go.jp

Method: uni-directional, sequence direction: sequenced from T3 primer

(5' -> 3')

Project: 'Silkworm Genome Program in MAFF, and Research for the

Future Program in JSPS'. see 'SilkBase',

<http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.

FEATURES

source

1. 584
 /organism="Bombyx mori"
 /strain="Shuko x Ryuhaku"
 /db_xref="taxon:7091"
 /clone="pg-0399"
 /clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku
 newly-enclosed adult"
 /sex="female"
 /tissue_type="pheromone gland"
 /dev_stage="newly-enclosed adult"
 167 a 133 c 151 g 133 t

BASE COUNT

ORIGIN

Query Match 31.1%; Score 379; DB 9; Length 584;
 Best Local Similarity 97.5%; Pred. No. 9.8e-98;
 Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 423 CCGAAATCGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 482
 Db 117 CCGAAATCGCAAAATCCCTTATAAATCAAAAGATAGCCCGAGATAGGTTGAGTGTG 176
 QY 483 TTCCAGTTTGAACAGAGTCCACTATTAAAGAGCTGGACTCCCAAGTCAAGGCGAA 542
 Db 177 TTCCAGTTTGAACAGAGTCCACTATTAAAGAGCTGGACTCCCAAGTCAAGGCGAA 236
 QY 543 AAACCGTCTATCAGGGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTGG 602
 Db 237 AAACCGTCTATCAGGGGATGGCCCACTACGTGAACCATCACCCAAATCAAGTTTTTGG 296
 QY 603 GGTGAGGTGCGGTAAGAGCTAAATCGAACCCCTAAAGGAGAGCCCGGATTTAGAGCTT 662
 Db 297 GGTGAGGTGCGGTAAGAGCTAAATCGAACCCCTAAAGGAGAGCCCGGATTTAGAGCTT 356
 QY 663 GACGGGAAAGCGCGCAAGTGTAGCGGTACGCTGCGCGTAAACCAACACCCGCGCGCTTA 722
 Db 357 GACGGGAAAGCGCGCAAGTGTAGCGGTACGCTGCGCGTAAACCAACACCCGCGCGCTTA 416
 QY 723 CTAGGCGCTGCGCAAGTGTAGCGGTACGCTGCGCGTAAACCAACACCCGCGCGCTTA 782
 Db 417 CTAGGCGCTGCGCAAGTGTAGCGGTACGCTGCGCGTAAACCAACACCCGCGCGCTTA 476
 QY 783 ATGCGCGCTACAGGGCGCGTACTATGTTGCTTT 817
 Db 477 ATGCGCGCTACAGGGCGCGTACTATGTTGCTTT 511

RESULT 14

AV403998

LOCUS

AV403998 Bombyx mori pheromone gland Shuko x Ryuhaku linear EST 06-FEB-2000
 adult Bombyx mori cDNA clone pg-0317 T3, mRNA sequence.

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

Bombyx mori cDNA

JOURNAL
COMMENT

Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
method: uni-directional, sequence direction: sequenced from T3 primer
(5' -> 3')
Project= 'Silkworm Genome Program in MAFF, and Research for the
Future Program in JSPS', see 'SilkBase',
<http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.

FEATURES

source

1. 627
Location/Qualifiers
/organism="Bombyx mori"
/strain="Shuko x Ryuhaku"
/db_xref="taxon:7091"
/clone="pg-0317"
/clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku
newly-eclosed adult"
/sex="female"
/tissue_type="pheromone gland"
/dev_stage="newly-eclosed adult"

BASE COUNT
ORIGIN

188 a 137 c 158 g 144 t

Query Match 31.1%; Score 379; DB 9; Length 627;

Best Local Similarity 97.5%; Pred. No. 1e-97;

Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 423 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTG 482
|||||
Db 116 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTG 175
QY 483 TTCAGTTTGGACAAAGTCCACTATTAAGAAGCTGACCTCAAGTCCTCAAGAGGCGAA 542
Db 176 TTCAGTTTGGACAAAGTCCACTATTAAGAAGCTGACCTCAAGTCCTCAAGAGGCGAA 235
QY 543 AAACCGTCTATCAGGCGGATGGCCACTACGTGAACCATCACCCAAATCAAGTTTGG 602
Db 236 AAACCGTCTATCAGGCGGATGGCCACTACGTGAACCATCACCCAAATCAAGTTTGG 295
QY 603 GGTGAGGTCCGTAAAGCACTAAATCGGAACCTAAAGGAGCGCCCGATTAGAGCTT 662
Db 296 GGTGAGGTCCGTAAAGCACTAAATCGGAACCTAAAGGAGCGCCCGATTAGAGCTT 355
QY 663 GACGGGAAAGCCGCGCAACGTGCGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
Db 356 GACGGGAAAGCCGCGCAACGTGCGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 415
QY 723 CTAGGGGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCCGCGCTTA 782
Db 416 CTAGGGGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCCGCGCTTA 475
QY 783 ATGCGCGCTACAGGGCGCGCTACTATGTTGCTTT 817
Db 476 ATGCGCGCTACAGGGCGCGCTAGTGGCACTTTT 510

RESULT 15

AV404060

LOCUS

AV404060 Bombyx mori pheromone gland Shuko x Ryuhaku linear EST 06-FEB-2000
adult Bombyx mori cDNA clone pg-0393 T3, mRNA sequence.

DEFINITION

AV404060

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bombyx mori

domestic silkworm.

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia

; Bombycoidea; Bombycidae; Bombyx.

1 (bases 1 to 627)

AUTHORS
TITLE
JOURNAL
COMMENT

Mita, K., Morimyo, M., Shimada, T., Okano, K. and Maeda, S.
Bombyx mori cDNA
Unpublished (2000)
Contact: Mita K
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
method: uni-directional, sequence direction: sequenced from T3 primer
(5' -> 3')
Project= 'Silkworm Genome Program in MAFF, and Research for the
Future Program in JSPS', see 'SilkBase',
<http://www.ab.a.u-tokyo.ac.jp/silkbase/>, for whole ESTdb.

FEATURES

source

1. 627
Location/Qualifiers
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/strain="Shuko x Ryuhaku"
/db_xref="taxon:7091"
/clone="pg-0393"
/clone_lib="Bombyx mori pheromone gland Shuko x Ryuhaku
newly-eclosed adult"
/sex="female"
/tissue_type="pheromone gland"
/dev_stage="newly-eclosed adult"

BASE COUNT
ORIGIN

188 a 137 c 158 g 144 t

Query Match 31.1%; Score 379; DB 9; Length 627;

Best Local Similarity 97.5%; Pred. No. 1e-97;

Matches 385; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 423 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTG 482
Db 116 CCGAAATCGGCAAAATCCCTTATAAATCAAAAGAAATAGCCGAGATAGGGTTGAGTGTG 175
QY 483 TTCAGTTTGGACAAAGTCCACTATTAAGAAGCTGACCTCAAGTCCTCAAGAGGCGAA 542
Db 176 TTCAGTTTGGACAAAGTCCACTATTAAGAAGCTGACCTCAAGTCCTCAAGAGGCGAA 235
QY 543 AAACCGTCTATCAGGCGGATGGCCACTACGTGAACCATCACCCAAATCAAGTTTGG 602
Db 236 AAACCGTCTATCAGGCGGATGGCCACTACGTGAACCATCACCCAAATCAAGTTTGG 295
QY 603 GGTGAGGTCCGTAAAGCACTAAATCGGAACCTAAAGGAGCGCCCGATTAGAGCTT 662
Db 296 GGTGAGGTCCGTAAAGCACTAAATCGGAACCTAAAGGAGCGCCCGATTAGAGCTT 355
QY 663 GACGGGAAAGCCGCGCAACGTGCGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 722
Db 356 GACGGGAAAGCCGCGCAACGTGCGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGG 415
QY 723 CTAGGGGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCCGCGCTTA 782
Db 416 CTAGGGGCTGGCAAGTGTAGCGGTACGCTGCGGTAAACCAACACCCCGCGCTTA 475
QY 783 ATGCGCGCTACAGGGCGCGCTACTATGTTGCTTT 817
Db 476 ATGCGCGCTACAGGGCGCGCTAGTGGCACTTTT 510

Search completed: August 1, 2002, 08:39:40

Job time: 6471 sec

